68603

Delaval, Jan

From: Roark, Jessica
Sent: Wednesday, June 12, 2002 10:45 AM
To: Delaval, Jan
Subject: 09/780035

Jan,

Please search the following from 09/780,035 in all protein databases

SEQ ID NOS:9-14.

Results on paper please.

Thanks!

Jessica H. Roark

CM1 9D04
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:18:15 ; Search time 136.11 Seconds
(without alignments)
4.896 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	100.0	6	22	AAB50794	Murine antibody S2
2	37	100.0	6	22	AAG65299	Anti-IL-18 antibod
3	37	100.0	113	22	AAG65308	Anti-IL-18 antibod
4	37	100.0	113	22	AAG65352	Anti-IL-18 antibod
5	37	100.0	114	22	AAB50793	Murine antibody S2
6	37	100.0	121	22	AAE03752	Murine PSCA Ab hea
7	37	100.0	123	22	AAU02587	Anti-adipocyte mon
8	37	100.0	222	22	AAE03757	Chimeric antibody
9	37	100.0	1471	22	ABB58739	Drosophila melanog
10	36	97.3	608	22	ABB64278	Drosophila melanog
11	34	91.9	114	16	AAR79244	Heavy chain variab
12	34	91.9	117	16	AAR66296	Human immunoglobul
13	34	91.9	123	19	AAW79228	Heavy chain variab
14	34	91.9	124	21	AAY87655	Murine PIP3 recogn
15	34	91.9	146	18	AAW22841	Human anti-tumour
16	34	91.9	148	21	AAY96295	Human IGFAM-7 immu
17	34	91.9	243	15	AAR60781	Fv(GP-4) immunosup
18	34	91.9	243	20	AAY42294	Anti-5T4 secreted
19	34	91.9	243	20	AAY27407	5T4 scFv antibody
20	34	91.9	243	20	AAW86002	Murine anti-5T4 an
21	34	91.9	243	22	AAB83835	Amino acid sequenc
22	34	91.9	488	20	AAW86004	Human B7-1.5T4.1 p
23	34	91.9	488	22	AAB83836	Amino acid sequenc
24	34	91.9	592	22	AAB83838	Amino acid sequenc
25	34	91.9	595	20	AAW86003	Anti-5T4 single ch
26	33	89.2	115	22	AAO00404	Human polypeptide
27	33	89.2	126	21	AAB21359	Rat antibody 2C10
28	32	86.5	92	21	AAG45009	Zea mays protein f
29	32	86.5	109	22	AAM95742	Human reproductive
30	32	86.5	125	21	AAG45008	Zea mays protein f
31	32	86.5	131	21	AAG18408	Arabidopsis thalia
32	32	86.5	136	20	AAY06579	Arabidopsis thalia
33	32	86.5	169	21	AAG42313	Arabidopsis thalia
34	32	86.5	221	21	AAG20197	Arabidopsis thalia
35	32	86.5	248	21	AAG46650	Arabidopsis thalia
36	32	86.5	249	21	AAG46649	Arabidopsis thalia
37	32	86.5	253	21	AAG46648	Arabidopsis thalia
38	32	86.5	288	20	AAW82743	Fusion protein pNG
39	32	86.5	350	22	ABB63707	Drosophila melanog
40	32	86.5	445	16	AAR76085	MAb 55.1 heavy cha
41	32	86.5	464	16	AAR76088	MAb 55.1 heavy cha
42	32	86.5	585	22	AAE12810	Wheat arginyl-tRNA
43	32	86.5	611	22	AAE12809	Soybean arginyl-tR
44	32	86.5	673	20	AAW82742	Plasmid pNG4/55.1s
45	32	86.5	915	22	ABB70955	Drosophila melanog

ALIGNMENTS

RESULT 1
AAB50794
ID AAB50794 standard; Protein; 6 AA.
XX
AC AAB50794;
XX
DT 21-MAR-2001 (first entry)
XX
DE Murine antibody S2C6 heavy chain variable region CDR1.
XX
KW Mouse; antibody; S2C6; heavy chain variable region; CD40; cancer;
KW inflammatory disease; immune system disorder; CDR;
KW complementarity determining region.
XX
OS Mus musculus.
XX
PN WO200075348-A1.
XX
PD 14-DEC-2000.
XX
PF 08-JUN-2000; 2000WO-US15749.
XX
PR 08-JUN-1999; 99US-0328296.
XX
PA (SEAT-) SEATTLE GENETICS INC.
XX
PI Siegall CB, Wahl AF, Francisco JA, Fell HP;
XX
DR WPI; 2001-071080/08.
XX
PT Anti-CD40 antibodies which immunospecifically bind CD40, useful for
PT prevention and treatment of cancer, inflammatory diseases and disorders
PT or deficiencies of immune system -
XX

PS Claim 1; Page 88; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC anti-CD40 antibodies. These can be used in the treatment of cancer and
CC inflammatory and immune system diseases, including systemic lupus
CC erythematosus, scleroderma, inflammatory myositis, Sjogren's syndrome,
CC mixed connective tissue disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease, acute respiratory distress
CC syndrome, pulmonary inflammation, osteoporosis, delayed type
CC hypersensitivity, asthma, primary biliary cirrhosis and idiopathic
CC thrombocytopaenic purpura.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 37; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 1 tgyyih 6

RESULT 2
AAG65299
ID AAG65299 standard; protein; 6 AA.
XX
AC AAG65299;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain CDR1 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 25; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain CDR1 fragment.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 37; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 1 tgyyih 6

RESULT 3
AAG65308
ID AAG65308 standard; protein; 113 AA.
XX
AC AAG65308;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47511.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory

CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain sequence.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 37; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 30 tgyyih 35

RESULT 4
AAG65352
ID AAG65352 standard; Protein; 113 AA.
XX
AC AAG65352;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47511.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 86; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 37; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 30 tgyyih 35

RESULT 5
AAB50793
ID AAB50793 standard; Protein; 114 AA.
XX
AC AAB50793;
XX
DT 21-MAR-2001 (first entry)
XX
DE Murine antibody S2C6 heavy chain variable region.
XX
KW Mouse; antibody; S2C6; heavy chain variable region; CD40; cancer;
KW inflammatory disease; immune system disorder.
XX
OS Mus musculus.
XX
PN WO200075348-A1.
XX
PD 14-DEC-2000.
XX
PF 08-JUN-2000; 2000WO-US15749.
XX
PR 08-JUN-1999; 99US-0328296.
XX
PA (SEAT-) SEATTLE GENETICS INC.
XX
PI Siegall CB, Wahl AF, Francisco JA, Fell HP;
XX
DR WPI; 2001-071080/08.
DR N-PSDB; AAC91890.
XX
PT Anti-CD40 antibodies which immunospecifically bind CD40, useful for
PT prevention and treatment of cancer, inflammatory diseases and disorders
PT or deficiencies of immune system -
XX
PS Claim 3; Fig 2; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC anti-CD40 antibodies. These can be used in the treatment of cancer and
CC inflammatory and immune system diseases, including systemic lupus
CC erythematosus, scleroderma, inflammatory myositis, Sjogren's syndrome,
CC mixed connective tissue disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease, acute respiratory distress
CC syndrome, pulmonary inflammation, osteoporosis, delayed type
CC hypersensitivity, asthma, primary biliary cirrhosis and idiopathic
CC thrombocytopaenic purpura.
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 37; DB 22; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 30 tgyyih 35

RESULT 6
AAE03752
ID AAE03752 standard; Protein; 121 AA.
XX

```
AC   AAE03752;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Murine PSCA Ab heavy chain variable region domain from clone 6B8.1D7.2B3.
XX
KW   Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
KW   glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
KW   heavy chain variable domain; VH.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          26..35
FT                   /label= CDR1
FT                   /note= "Complementarity determining region 1"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "Complementarity determining region 2"
FT   Region          99..103
FT                   /label= CDR3
FT                   /note= "Complementarity determining region 3"
XX
PN   WO200140309-A2.
XX
PD   07-JUN-2001.
XX
PF   27-OCT-2000; 2000WO-US29603.
XX
PR   29-OCT-1999;   99US-0162558.
PR   16-FEB-2000; 2000US-0182872.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Devaux B,  Keller G,  Koeppen H,  Lasky LA;
XX
DR   WPI; 2001-389954/41.
XX
PT   Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
PT   on binding to PSCA on mammalian cell and inhibits growth of
PT   PSCA-expressing cancer cells in vivo, useful for killing
PT   PSCA-expressing cancer cells  -
XX
PS   Claim 22; Fig 12; 112pp; English.
XX
CC   The present sequence is murine prostate stem cell antigen (PSCA)
CC   antibody (Ab) heavy chain variable region domain (VH) from hybridoma
CC   clone 6B8.1D7.2B3, Asc# 2761. PSCA is a single subunit glycoprotein that
CC   is expressed on the cell surface as a glycosylphosphatidylinositol (GPI)-
CC   anchored protein. The present invention relates to anti-PSCA antibody
CC   composition and methods of killing PSCA-expressing cancer cells. PSCA is
CC   useful for inhibiting and killing the growth of PSCA-expressing cancer
CC   cells such as prostate cancer, bladder cancer or lung cancer cells.
CC   Humanised antibody conjugated to a toxin or a radioactive isotope is used
CC   for killing the cancer cells. PSCA is useful for specifically targetting
CC   PSCA-expressing tumour cells in vivo and for inhibiting or killing these
CC   cells. The antibodies are also useful for treating the above mentioned
CC   cancers and for diagnosing and staging of PSCA-expressing cancer, for
CC   purification or immunoprecipitation of PSCA from cells, and for detection
CC   and quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC   cancers by gene therapy techniques.
XX
SQ   Sequence   121 AA;


  Query Match             100.0%;  Score 37;  DB 22;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||||
Db      30 tgyyih 35


RESULT   7
AAU02587
ID   AAU02587 standard; Protein; 123 AA.
XX
AC   AAU02587;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Anti-adipocyte monoclonal antibody heavy chain, FAT 74.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW   heart disease; complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO200127279-A1.
XX
PD   19-APR-2001.
XX
PF   11-OCT-2000; 2000WO-GB03900.
XX
PR   12-OCT-1999;   99US-0158812.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM,  Main SH,  Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   N-PSDB; AAS03487.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity
PT   related diseases -
XX
PS   Claim 1; Page 147; 182pp; English.
XX
CC   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC   sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC   chain, and heavy chain complementarity determining regions (CDR) of the
CC   invention. The antibodies can be used in the treatment of obesity and
CC   obesity related diseases. The antibodies can be used to deliver drugs or
CC   pro-drugs directly to the fat mass of an obese patient or the antibody
CC   can be used as a therapeutic itself. Antibodies binding specifically to
CC   adipocytes can be used to activate the immune system to destroy the cells
CC   by complement mediated lysis. The antibodies may be labeled with a
CC   detectable label such as radiolabel, fluorescent or chemical group and
CC   used in methods of diagnosis in human subjects e.g. to determine the
CC   presence of adipocyte antigen on the surface of an adipocyte to detect or
CC   determine the presence or level of adipocytes in a cell or tissue sample.
CC   The antibodies can be used as an alternative means of treatment for obese
CC   patients other than undergoing surgery to remove excess fat. Antibodies
CC   for different types of fat deposits can also be produced e.g. intra-
CC   abdominal fat associated with heart disease.
XX
SQ   Sequence   123 AA;


  Query Match             100.0%;  Score 37;  DB 22;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||||
Db      30 tgyyih 35


RESULT   8
AAE03757
ID   AAE03757 standard; Protein; 222 AA.
XX
AC   AAE03757;
XX
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```
DT   07-AUG-2001  (first entry)
XX
DE   Chimeric antibody 6B8 Fab heavy chain (6B8.1D7.2B3).
XX
KW   Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
KW   glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
KW   human; antibody binding fragment; Fab; heavy chain region.
XX
OS   Chimeric - Mus musculus.
OS   Chimeric - Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..115
FT                   /note= "Derived from mouse heavy chain variable
FT                   region (VH)"
FT   Region          116..222
FT                   /note= "Derived from human heavy chain constant
FT                   region"
XX
PN   WO200140309-A2.
XX
PD   07-JUN-2001.
XX
PF   27-OCT-2000; 2000WO-US29603.
XX
PR   29-OCT-1999;   99US-0162558.
PR   16-FEB-2000; 2000US-0182872.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Devaux B,  Keller G,  Koeppen H,  Lasky LA;
XX
DR   WPI; 2001-389954/41.
XX
PT   Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
PT   on binding to PSCA on mammalian cell and inhibits growth of
PT   PSCA-expressing cancer cells in vivo, useful for killing
PT   PSCA-expressing cancer cells  -
XX
PS   Claim 5; Fig 13; 112pp; English.
XX
CC   The present chimeric sequence is full length 2761 antibody binding
CC   fragment (Fab) heavy chain (6B8.1D7.2B3) derived from murine heavy
CC   chain variable region (VH) and human heavy chain constant region.
CC   This antibody binds to prostate stem cell antigen (PSCA) which is a
CC   single subunit glycoprotein that is expressed on the cell surface as a
CC   glycosylphosphatidylinositol (GPI)-anchored protein. The present
CC   invention relates to anti-PSCA antibody composition and methods of
CC   killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
CC   killing the growth of PSCA-expressing cancer cells such as prostate
CC   cancer, bladder cancer or lung cancer cells. Humanised antibody
CC   conjugated to a toxin or a radioactive isotope is used for killing the
CC   cancer cells. PSCA is useful for specifically targetting PSCA-expressing
CC   tumour cells in vivo and for inhibiting or killing these cells. The
CC   antibodies are also useful for treating the above mentioned cancers and
CC   for diagnosing and staging of PSCA-expressing cancer, for purification
CC   or immunoprecipitation of PSCA from cells, and for detection and
CC   quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC   cancers by gene therapy techniques.
XX
SQ   Sequence   222 AA;


  Query Match             100.0%;  Score 37;  DB 22;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||||
Db      30 tgyyih 35


RESULT   9
```

```
ABB58739
ID   ABB58739 standard; Protein; 1471 AA.
XX
AC   ABB58739;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 3009.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL02842.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 3009; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   1471 AA;


  Query Match             100.0%;  Score 37;  DB 22;  Length 1471;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||||
Db     679 tgyyih 684


RESULT  10
ABB64278
ID   ABB64278 standard; Protein; 608 AA.
XX
AC   ABB64278;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 19626.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
```

OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL08381.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 19626; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 608 AA;

Query Match 97.3%; Score 36; DB 22; Length 608;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 509 tgyyvh 514

ULT 11
79244
ID AAR79244 standard; Protein; 114 AA.
XX
AC AAR79244;
XX
DT 21-DEC-1995 (first entry)
XX
DE Heavy chain variable region for monoclonal antibody 23F8.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW heavy chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97501.
XX
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 13; Page 58; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAbs that were strongly positive
CC against glutatione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX
SQ Sequence 114 AA;

Query Match 91.9%; Score 34; DB 16; Length 114;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 24 tgyymh 29

RESULT 12
AAR66296
ID AAR66296 standard; Protein; 117 AA.
XX
AC AAR66296;
XX
DT 07-AUG-1995 (first entry)
XX
DE Human immunoglobulin variable heavy chain #2.
XX
KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX
OS Homo sapiens.
XX
PN WO9426895-A.
XX
PD 24-NOV-1994.
XX
PF 10-MAY-1993; 93WO-JP00603.
XX
PR 10-MAY-1993; 93WO-JP00603.
XX
PA (NISB) JAPAN TOBACCO INC.
XX

PI Honjo T, Matsuda F;
XX
DR WPI; 1995-006791/01.
DR N-PSDB; AAQ78940.
XX
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
XX
PS Disclosure; Page 32-33; 130pp; Japanese.
XX
CC Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
CC chain sequences encoded by novel isolated genes. The genes
CC (AAQ78939-79002) were isolated and cloned from a series of cosmid
CC constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
CC amplification using primers AAQ78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TaqI restriction enzyme.
CC The fragments were separated by gel elecrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
XX
SQ Sequence 117 AA;

Query Match 91.9%; Score 34; DB 16; Length 117;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||:|
Db 49 tgyymh 54

RESULT 13
AAW79228
ID AAW79228 standard; Protein; 123 AA.
XX
AC AAW79228;
XX
DT 21-DEC-1998 (first entry)
XX
DE Heavy chain variable region of human Amu 5-3.
XX
KW Monoclonal antibody; MAb; LO-CD2a; humanised antibody; chimeric;
KW T-cell; immune response; CD2 antigen;graft-versus-host disease;
KW human lymphocyte; transplant rejection; autoimmune disease; Amu 5-3.
XX
OS Homo sapiens.
XX
PN US5817311-A.
XX
PD 06-OCT-1998.
XX
PF 07-JUN-1995; 95US-0472281.
XX
PR 07-JUN-1995; 95US-0472281.
PR 05-MAR-1993; 93US-0027008.
PR 09-SEP-1993; 93US-0119032.
PR 29-MAR-1995; 95US-0407009.
XX
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Bazin H, Latinne D;
XX
DR WPI; 1998-556337/47.
XX
PT Inhibition of T-cell mediated immune response with anti-CD2
PT monoclonal antibody LO-CD2a - used for preventing transplant
PT rejection or for treating graft-versus-host disease or auto-immune
PT diseases
XX
PS Example 7; Fig 33; 96pp; English.
XX
CC This represents the amino acid sequence of the light chain variable
CC region of human antibody clone Amu 5-3. This is used to consruct a
CC humanised antibody LO-CD2a. The invention relates to the use of the
CC monoclonal antibody (MAb) LO-CD2a or a humanised or a chimeric version
CC of the LO-CD2a antibody for the inhibition of a T-cell mediated immune
CC response in a patient. The MAb LO-CD2a (produced by hybridoma cell line
CC ATCC HB 11423) can bind to an epitope on the CD2 antigen of the human
CC lymphocytes. The T-cell mediated immune response in a patient can be
CC inhibited by administering the MAb LO-CD2a or an antibody that binds to
CC the same human lymphocyte epitope as LO-CD2a. The method is used for
CC preventing transplant rejection or for treating graft-versus-host
CC disease or for treating autoimmune diseases.
XX
SQ Sequence 123 AA;

Query Match 91.9%; Score 34; DB 19; Length 123;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||:|
Db 30 tgyymh 35

RESULT 14
AAY87655
ID AAY87655 standard; Protein; 124 AA.
XX
AC AAY87655;
XX
DT 11-AUG-2000 (first entry)
XX
DE Murine PIP3 recognizing Mab variable region heavy chain protein.
XX
KW PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;
KW immunogen; antibody; heavy chain.
XX
OS Mus sp.
XX
PN JP2000083664-A.
XX
PD 28-MAR-2000.
XX
PF 07-SEP-1998; 98JP-0252921.
XX
PR 07-SEP-1998; 98JP-0252921.
XX
PA (FUKU/) FUKUI Y.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
DR WPI; 2000-353334/31.
DR N-PSDB; AAA12202.
XX
PT A monoclonal antibody recognizing
PT phosphatidylinositol-3,4,5-triphosphate -
XX
PS Claim 5; Page 11; 15pp; Japanese.
XX
CC This invention describes a novel antibody specifically recognizing
CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the
CC invention is used in immunogenic compositions in which a dead
CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The
CC antibody can be used in an immunoassay containing a step in which the
CC above antibody or its variable region is reacted with PIP3 present in a
CC sample and the bond based on their immunological reaction. The method
CC can determine PIP3 easily in a high sensitivity. This sequence represents
CC the murine PIP3 recognizing monoclonal antibody variable region heavy
CC chain described in the method of the invention.

XX
SQ Sequence 124 AA;

Query Match 91.9%; Score 34; DB 21; Length 124;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||:|
Db 30 tgyymh 35

RESULT 15
AAW22841
ID AAW22841 standard; Protein; 146 AA.
XX
AC AAW22841;
XX
DT 12-SEP-1997 (first entry)

[redacted]

Human anti-tumour antigen antibody heavy chain variable region.
XX
KW Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;
KW variable region; medicine; pharmacology; biochemistry; CDR;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Peptide 20..146
FT /label= mat_peptide
FT Region 50..54
FT /label= CDR_1
FT Region 69..85
FT /label= CDR_2
FT Region 118..139
FT /label= CDR_3
XX
PN JP09100300-A.
XX
PD 15-APR-1997.
XX
PF 03-OCT-1995; 95JP-0278266.
XX
PR 03-OCT-1995; 95JP-0278266.

[redacted]

(HAGI/) HAGIWARA Y.
XX
DR WPI; 1997-276726/25.
DR N-PSDB; AAT75422.
XX
PT Anticancer human monoclonal antibody variable region sequences - and
PT related DNA and RNA
XX
PS Claim 3; Page 10; 14pp; Japanese.
XX
CC The present sequence is a human anti-tumour antigen
CC monoclonal antibody (MAb) heavy chain variable region, useful in
CC medicine, pharmacology and biochemistry. The isotype of a MAb
CC secreted by the human/human hybridoma HT was determined to be mu
CC and kappa. Human MAb was purified, and the antigen recognised by
CC human MAb CLN"-IgM identified by western blotting.
XX
SQ Sequence 146 AA;

Query Match 91.9%; Score 34; DB 18; Length 146;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||:|
Db 49 tgyymh 54

Search completed: June 12, 2002, 11:23:31
Job time: 316 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:36 ; Search time 29.47 Seconds
(without alignments)
7.883 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

T[redacted] number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	91.9	117	1	HV1G_HUMAN	P23083 homo sapien
2	33	89.2	231	1	Y493_RICPR	Q9zd54 rickettsia
3	33	89.2	524	1	VL2_HPV17	P36751 human papil
4	32	86.5	87	1	VPR_HV2BE	P18100 human immun
5	32	86.5	182	1	GRPE_AQUAE	O66745 aquifex aeo
6	32	86.5	209	1	RANA_LOTJA	P54765 lotus japon
7	32	86.5	209	1	RANB_LOTJA	P54766 lotus japon
8	32	86.5	221	1	RAN1_ARATH	P41916 arabidopsis
9	32	86.5	221	1	RAN1_LYCES	P38546 lycopersico
10	32	86.5	221	1	RAN2_ARATH	P41917 arabidopsis
11	32	86.5	221	1	RAN2_LYCES	P38547 lycopersico
12	32	86.5	221	1	RANA_TOBAC	P41918 nicotiana t
13	32	86.5	221	1	RANB_TOBAC	P41919 nicotiana t
14	32	86.5	221	1	RAN_VICFA	P38548 vicia faba
15	32	86.5	632	1	ATE1_ARATH	Q9zt48 arabidopsis
16	31	83.8	590	1	HMDF_DROME	P07548 drosophila
17	31	83.8	643	1	VP4B_VACCV	P06440 vaccinia vi
18	31	83.8	644	1	VP4B_VACCC	P20643 vaccinia vi
19	31	83.8	644	1	VP4B_VARV	P33818 variola vir
20	30	81.1	195	1	TRIN_SULTO	Q973j1 sulfolobus
21	30	81.1	232	1	EV2A_HUMAN	P22794 homo sapien
22	30	81.1	263	1	YC56_PORPU	P51208 porphyra pu
23	30	81.1	289	1	SOXR_ARTSP	Q44311 arthrobacte
24	30	81.1	324	1	YPDA_BACSU	P50736 bacillus su
25	30	81.1	420	1	DHE3_PYRKO	O59650 pyrococcus
26	30	81.1	486	1	PHOQ_ECOLI	P23837 escherichia
27	30	81.1	487	1	PHOQ_SALTY	P14147 salmonella
28	30	81.1	638	1	SCAD_HUMAN	P51172 homo sapien
29	30	81.1	638	1	SCAD_PANTR	O46547 pan troglod
30	30	81.1	762	1	AOCY_BOVIN	O46406 bos taurus
31	30	81.1	846	1	PAC_ECOLI	P06875 escherichia
32	30	81.1	5376	1	ZAN_MOUSE	O88799 mus musculu
33	29	78.4	168	1	PFD5_DROME	Q9vcz8 drosophila
34	29	78.4	312	1	DHBK_MOUSE	O70503 mus musculu
35	29	78.4	314	1	MIAA_CHLMU	Q9p1f7 chlamydia m
36	29	78.4	314	1	MIAA_CHLTR	O84771 chlamydia t
37	29	78.4	317	1	YG00_HAEIN	P44268 haemophilus
38	29	78.4	340	1	MYMS_BOVIN	P80473 bos taurus
39	29	78.4	496	1	ERG1_CANAL	Q92206 candida alb
40	29	78.4	512	1	ER24_SEPLY	O13597 septoria ly
41	29	78.4	591	1	SYFB_CAEEL	Q19713 caenorhabdi
42	29	78.4	919	1	RPO2_CAPVK	P16716 capripoxvir
43	29	78.4	1451	1	MYM1_HUMAN	P52179 homo sapien
44	29	78.4	1666	1	MYM1_MOUSE	Q62234 mus musculu
45	29	78.4	3038	1	TRIO_HUMAN	O75962 homo sapien

ALIGNMENTS

```
RESULT   1
HV1G_HUMAN
ID   HV1G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V-I REGION V35.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13009 MW;  BE61CE63F8CE97BD CRC64;


  Query Match             91.9%;  Score 34;  DB 1;  Length 117;
  Best Local Similarity   83.3%;  Pred. No. 2.5;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||:|
Db      49 TGYYMH 54


RESULT   2
Y493_RICPR
ID   Y493_RICPR     STANDARD;      PRT;   231 AA.
AC   Q9ZD54;
DT   16-OCT-2001 (Rel. 40, Created)
```

```
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical aldolase class II protein RP493.
GN   RP493.
OS   Rickettsia prowazekii.
OC   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MADRID E;
RX   MEDLINE=99039499; PubMed=9823893;
RA   Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA   Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT   "The genome sequence of Rickettsia prowazekii and the origin of
RT   mitochondria.";
RL   Nature 396:133-140(1998).
CC   -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AJ235272; CAA14945.1; -.
DR   InterPro; IPR001303; Aldolase_II.
DR   Pfam; PF00596; Aldolase_II; 1.
KW   Hypothetical protein; Zinc; Complete proteome.
FT   METAL        94     94       ZINC (BY SIMILARITY).
FT   METAL        96     96       ZINC (BY SIMILARITY).
FT   METAL       158    158       ZINC (BY SIMILARITY).
SQ   SEQUENCE   231 AA;  26849 MW;  F48D03ADCB36D0D8 CRC64;


  Query Match             89.2%;  Score 33;  DB 1;  Length 231;
  Best Local Similarity   83.3%;  Pred. No. 8;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          |||:||
Db     74 TGYFIH 79


ULT   3
_HPV17
ID   VL2_HPV17      STANDARD;      PRT;   524 AA.
AC   P36751;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Minor capsid protein L2.
GN   L2.
OS   Human papillomavirus type 17.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10607;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94265501; PubMed=8205838;
RA   Delius H., Hofmann B.;
RT   "Primer-directed sequencing of human papillomavirus types.";
RL   Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X74469; CAA52516.1; -.
DR   PIR; S36483; S36483.
DR   InterPro; IPR000784; Late_L2.
DR   Pfam; PF00513; late_protein_L2; 1.
KW   Coat protein; Late protein.
SQ   SEQUENCE   524 AA;  56865 MW;  7EDAFC17F7EBD9C5 CRC64;


  Query Match             89.2%;  Score 33;  DB 1;  Length 524;
  Best Local Similarity   83.3%;  Pred. No. 19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||:|||
Db    476 TGFYIH 481


RESULT   4
VPR_HV2BE
ID   VPR_HV2BE      STANDARD;      PRT;    87 AA.
AC   P18100;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-JUL-1993 (Rel. 26, Last annotation update)
DE   VPR protein (R ORF protein).
GN   VPR.
OS   Human immunodeficiency virus type 2 (isolate BEN) (HIV-2).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11714;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90281594; PubMed=2353457;
RA   Kirchhoff F., Jentsch K., Bachmann B., Stuke A., Laloux C.,
RA   Lueke W., Stahl-Henning C., Schneider J., Nieselt K., Eigen M.,
RA   Hunsmann G.;
RT   "A novel proviral clone of HIV-2: biological and phylogenetic
RT   relationship to other primate immunodeficiency viruses.";
RL   Virology 177:305-311(1990).
CC   -!- MISCELLANEOUS: THIS ISOLATE IS FROM A GERMAN AIDS PATIENT (WITH
CC       PREDOMINANTLY NEUROLOGICAL COMPLICATIONS) WHO WAS PROBABLY
CC       INFECTED IN MALI.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M30502; AAB00740.1; -.
DR   HIV; M30502; VPR$2BEN.
DR   InterPro; IPR000012; HIV_ORFXR.
DR   Pfam; PF00522; VPR; 1.
DR   PRINTS; PR00444; HIVVPRVPX.
KW   AIDS.
SQ   SEQUENCE   87 AA;  10071 MW;  CB3424E9A4171DA5 CRC64;


  Query Match             86.5%;  Score 32;  DB 1;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 4.8;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 GYYIH 6
          |||||
Db     48 GYYIH 52


RESULT   5
GRPE_AQUAE
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:36 ; Search time 107.96 Seconds
(without alignments)
9.614 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

T number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	100.0	206	12	Q65297	Q65297 amapari vir
2	37	100.0	558	12	Q84169	Q84169 oliveros vi
3	37	100.0	1471	5	Q9VA99	Q9va99 drosophila
4	36	97.3	218	5	O15936	O15936 aedes aegyp
5	36	97.3	608	5	Q9VMM5	Q9vmm5 drosophila
6	34	91.9	119	4	Q9UL94	Q9ul94 homo sapien
7	34	91.9	125	4	Q9UL95	Q9ul95 homo sapien
8	33	89.2	231	16	Q92HU3	Q92hu3 rickettsia
9	32	86.5	114	10	Q42161	Q42161 arabidopsis
10	32	86.5	133	10	Q947D3	Q947d3 prunus pers
11	32	86.5	170	10	Q9ZPJ5	Q9zpj5 zea mays (m
12	32	86.5	221	10	O22495	O22495 arabidopsis
13	32	86.5	221	10	Q9XJ44	Q9xj44 oryza sativ
14	32	86.5	221	10	Q9FSZ5	Q9fsz5 cicer ariet
15	32	86.5	221	10	Q9XJ45	Q9xj45 oryza sativ
16	32	86.5	221	10	O04148	O04148 arabidopsis
17	32	86.5	221	10	O04664	O04664 arabidopsis
18	32	86.5	221	10	Q94K33	Q94k33 arabidopsis
19	32	86.5	221	10	Q944C6	Q944c6 triticum ae
20	32	86.5	350	5	Q9VHF2	Q9vhf2 drosophila
21	32	86.5	361	3	O14133	O14133 schizosacch
22	32	86.5	408	12	Q9J575	Q9j575 fowlpox vir
23	32	86.5	416	5	P90914	P90914 caenorhabdi
24	32	86.5	421	16	Q9JYQ5	Q9jyq5 neisseria m
25	32	86.5	421	16	Q9JTP6	Q9jtp6 neisseria m
26	32	86.5	605	10	Q9C776	Q9c776 arabidopsis
27	32	86.5	628	12	O90139	O90139 mamestra br
28	32	86.5	747	5	Q20046	Q20046 caenorhabdi
29	32	86.5	807	10	Q9C7K4	Q9c7k4 arabidopsis
30	32	86.5	915	5	Q9VDK3	Q9vdk3 drosophila
31	31	83.8	151	2	Q9RD46	Q9rd46 streptomyce
32	31	83.8	157	4	O95978	O95978 homo sapien
33	31	83.8	232	5	Q20030	Q20030 caenorhabdi
34	31	83.8	241	12	Q9J572	Q9j572 fowlpox vir
35	31	83.8	272	2	Q9L1D0	Q9l1d0 streptomyce
36	31	83.8	272	8	Q33574	Q33574 trypanosoma
37	31	83.8	307	16	Q9LCT4	Q9lct4 pseudomonas
38	31	83.8	311	17	O27048	O27048 methanother
39	31	83.8	347	8	Q34096	Q34096 crithidia f
40	31	83.8	369	17	Q9Y9L9	Q9y919 aeropyrum p
41	31	83.8	437	12	Q89223	Q89223 variola vir
42	31	83.8	449	5	Q20031	Q20031 caenorhabdi
43	31	83.8	451	5	Q21801	Q21801 caenorhabdi
44	31	83.8	459	10	Q9SYY3	Q9syy3 arabidopsis
45	31	83.8	460	10	Q9LZJ3	Q9lzj3 arabidopsis

ALIGNMENTS

```
RESULT   1
Q65297
ID   Q65297      PRELIMINARY;      PRT;   206 AA.
AC   Q65297;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NUCLEOCAPSID PROTEIN (FRAGMENT).
OS   Amapari virus.
OC   Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX   NCBI_TaxID=45218;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BEAN 70563;
RX   MEDLINE=96204598; PubMed=8623541;
RA   Bowen M.D., Peters C.J., Nichol S.T.;
RT   "The phylogeny of New World (Tacaribe complex) arenaviruses.";
RL   Virology 219:285-290(1996).
DR   EMBL; U43685; AAC54828.1; -.
DR   InterPro; IPR000229; Arena_nucleocap.
DR   Pfam; PF00843; Arena_nucleocap; 1.
DR   ProDom; PD004728; Arena_nucleocap; 1.
FT   NON_TER       1      1
FT   NON_TER     206    206
SQ   SEQUENCE   206 AA;  23256 MW;  7D64BEB31DC74D0B CRC64;


  Query Match             100.0%;  Score 37;  DB 12;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
           ||||||
Db      85 TGYYIH 90


RESULT   2
Q84169
ID   Q84169      PRELIMINARY;      PRT;   558 AA.
```

```
AC   Q84169;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NUCLEOCAPSID PROTEIN.
OS   Oliveros virus.
OC   Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX   NCBI_TaxID=42764;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3229-1;
RX   MEDLINE=96177154; PubMed=8599223;
RA   Bowen M.D., Peters C.J., Mills J.N., Nichol S.T.;
RT   "Oliveros virus: a novel arenavirus from Argentina.";
RL   Virology 217:362-366(1996).
DR   EMBL; U34248; AAC54655.1; -.
DR   InterPro; IPR000229; Arena_nucleocap.
DR   InterPro; IPR001998; Xylose_isom.
DR   Pfam; PF00843; Arena_nucleocap; 1.
DR   ProDom; PD004728; Arena_nucleocap; 1.
DR   PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SQ   SEQUENCE   558 AA;  62154 MW;  3F617AA78396A3D7 CRC64;


  Query Match             100.0%;  Score 37;  DB 12;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||||
Db    398 TGYYIH 403


RESULT   3
Q9VA99
ID   Q9VA99      PRELIMINARY;      PRT;  1471 AA.
AC   Q9VA99;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CG2176 PROTEIN.
GN   CG2176.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003772; AAF57015.2; -.
DR   HSSP; P00442; 1CB4.
DR   FlyBase; FBgn0039750; CG2176.
SQ   SEQUENCE   1471 AA;  164755 MW;  503CC84AE99EB2FD CRC64;


  Query Match             100.0%;  Score 37;  DB 5;  Length 1471;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||||
Db    679 TGYYIH 684


RESULT   4
O15936
ID   O15936      PRELIMINARY;      PRT;  218 AA.
AC   O15936;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HEXAMERIN 2 BETA (FRAGMENT).
GN   AAHEX-2B.
OS   Aedes aegypti (Yellowfever mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC   Aedes.
OX   NCBI_TaxID=7159;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ROCK STRAIN;
RA   Gordadze A.V., Korochkina S.E., Zakharkin S.O., Norton A.L., Benes H.;
RT   "Molecular cloning and expression of two hexamerins from Aedes
RT   aegypti.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF010132; AAB64174.1; -.
DR   HSSP; P04253; 1LLA.
DR   InterPro; IPR000896; Hemocyanin.
DR   Pfam; PF00372; hemocyanin; 1.
FT   NON_TER       1      1
FT   NON_TER     218    218
SQ   SEQUENCE   218 AA;  26026 MW;  B72A1BA6D2A82EB3 CRC64;


  Query Match             97.3%;  Score 36;  DB 5;  Length 218;
  Best Local Similarity   83.3%;  Pred. No. 19;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db    182 TGYYVH 187


RESULT   5
Q9VMM5
ID   Q9VMM5      PRELIMINARY;      PRT;  608 AA.
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:20:35 ; Search time 61.61 Seconds
(without alignments)
9.358 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

[redacted] number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	100.0	104	2	S69899	Ig heavy chain V r
2	37	100.0	105	2	S67941	Ig heavy chain var
3	37	100.0	120	2	A49982	Ig heavy chain V r
4	36	97.3	108	2	PH0977	Ig heavy chain V r
5	35	94.6	126	2	I44151	Ig heavy chain V r
6	34	91.9	98	2	S26938	Ig heavy chain V r
7	34	91.9	98	2	S26912	Ig heavy chain V r
8	34	91.9	105	2	PH0978	Ig heavy chain V r
9	34	91.9	107	2	S26320	Ig heavy chain V r
10	34	91.9	109	2	PH1668	Ig heavy chain V r
11	34	91.9	110	2	PH1669	Ig heavy chain V r
12	34	91.9	117	1	HVHU35	Ig heavy chain pre
13	34	91.9	117	2	S18551	Ig heavy chain V r
14	34	91.9	118	2	S36265	Ig heavy chain V r
15	34	91.9	129	2	S46393	Ig heavy chain V r
16	34	91.9	135	2	S49530	anti-Sm antibody V
17	33	89.2	231	2	G71652	erythrocyte adduci
18	33	89.2	231	2	F97784	erythrocyte adduci
19	33	89.2	524	2	S36483	L2 protein - human
20	32	86.5	182	2	E70339	heat shock protein
21	32	86.5	221	2	S46498	GTP-binding protei
22	32	86.5	361	2	T38693	probable trna prot
23	32	86.5	416	2	T23383	hypothetical prote
24	32	86.5	421	2	B81864	probable glutamate
25	32	86.5	421	2	B81079	glutamate dehydrog
26	32	86.5	629	2	T51729	arginine-tRNA-prot
27	32	86.5	747	2	T16274	hypothetical prote
28	32	86.5	807	2	F96604	protein F14G9.10 [
29	31	83.8	104	2	S26466	Ig heavy chain V r
30	31	83.8	112	2	S26473	Ig heavy chain V r
31	31	83.8	117	2	S09960	Ig heavy chain V-D
32	31	83.8	126	2	S58121	Ig heavy chain V r
33	31	83.8	138	2	S21810	Ig heavy chain V r
34	31	83.8	232	2	T16258	hypothetical prote
35	31	83.8	258	2	E97453	surfeit 1 (AF18295
36	31	83.8	258	2	AG2671	surfeit 1 [importe
37	31	83.8	288	2	A05235	hypothetical prote
38	31	83.8	307	2	E83093	hypothetical prote
39	31	83.8	311	2	D69229	conserved hypothet
40	31	83.8	328	2	AH1894	hypothetical prote
41	31	83.8	347	2	F22845	hypothetical prote
42	31	83.8	369	2	A72453	hypothetical prote
43	31	83.8	449	2	T16259	hypothetical prote
44	31	83.8	451	2	T24018	hypothetical prote
45	31	83.8	459	2	H85031	probable glycosylt

ALIGNMENTS

RESULT 1
S69899
Ig heavy chain V region (clone RFTS7H), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69899
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune re
A;Reference number: S69896; MUID:93272805
A;Accession: S69899
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-104 <RAN>
A;Cross-references: EMBL:Z34893; NID:g509803; PIDN:CAA84376.1; PID:g509804
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 37; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 30 TGYYIH 35

RESULT 2
S67941
Ig heavy chain variable region, subgroup I (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 30-May-1997
C;Accession: S67941
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a huma
A;Reference number: S67940; MUID:92314301
A;Accession: S67941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105 <HEX>
A;Cross-references: EMBL:X73851
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 37; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||

```
Db      12 TGYYIH 17


RESULT   3
A49982
Ig heavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: A49982
R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R
J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051
A;Accession: A49982
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <LIN>
A;Cross-references: GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 37;  DB 2;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
            ||||||
Db      30 TGYYIH 35


RESULT   4
PH0977
Ig heavy chain V region (clone 10-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0977
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444
A;Accession: PH0977
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             97.3%;  Score 36;  DB 2;  Length 108;
  Best Local Similarity   83.3%;  Pred. No. 2.9;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
            ||||:|
Db      30 TGYYVH 35


RESULT   5
I44151
Ig heavy chain V region (BO) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999
C;Accession: I44151
R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746
A;Accession: I44151
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-126 <ZEB>
A;Cross-references: GB:M88309; NID:g183952; PIDN:AAA35967.1; PID:g183953
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-99/Domain: immunoglobulin homology <IMM>


  Query Match             94.6%;  Score 35;  DB 2;  Length 126;
  Best Local Similarity   83.3%;  Pred. No. 5.5;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
            ||||:|
Db      31 TGYYLH 36


RESULT   6
S26938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 98;
  Best Local Similarity   83.3%;  Pred. No. 6.7;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
            ||||:|
Db      30 TGYYMH 35


RESULT   7
S26912
Ig heavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117
A;Accession: S26912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID:g32980
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 98;
  Best Local Similarity   83.3%;  Pred. No. 6.7;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGYYIH 6
```

```
          ||||:|
Db     30 TGYYMH 35


RESULT   8
PH0978
Ig heavy chain V region (clone 17s.166) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0978
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444
A;Accession: PH0978
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-105 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-97/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 105;
  Best Local Similarity   83.3%;  Pred. No. 7.2;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     29 TGYYMH 34


RESULT   9
S26320
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26320
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Accession: S26320
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <STA>
A;Cross-references: EMBL:X59206
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 107;
  Best Local Similarity   83.3%;  Pred. No. 7.4;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     18 TGYYMH 23


RESULT  10
PH1668
Ig heavy chain V region (clone 3G5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1668
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610
A;Accession: PH1668
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 109;
  Best Local Similarity   83.3%;  Pred. No. 7.5;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     22 TGYYMH 27


RESULT  11
PH1669
Ig heavy chain V region (clone 3B2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1669
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staph
A;Reference number: PH1642; MUID:93301610
A;Accession: PH1669
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>


  Query Match             91.9%;  Score 34;  DB 2;  Length 110;
  Best Local Similarity   83.3%;  Pred. No. 7.6;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     22 TGYYMH 27


RESULT  12
HVHU35
Ig heavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: S00476; S34013
R;Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fuk
EMBO J. 7, 1047-1051, 1988
A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain
A;Reference number: S00476; MUID:88296408
A;Accession: S00476
A;Molecule type: DNA
A;Residues: 1-117 <MATS>
A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Note: the authors translated the codon AGT for residue 89 as Met
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclon
A;Reference number: S34001; MUID:93209281
A;Accession: S34013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
A;Introns: 16/1
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 34; DB 1; Length 117;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 49 TGYYMH 54

RESULT 13
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524
A;Accession: S18551
A;Molecule type: DNA
A;Residues: 1-117 <SHI>
A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804
A;Accession: S23625
A;Molecule type: DNA
A;Residues: 1-117 <OLE>
A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 34; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 49 TGYYMH 54

RESULT 14
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 34; DB 2; Length 118;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 30 TGYYMH 35

RESULT 15
S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage
A;Reference number: S46390; MUID:94254092
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 34; DB 2; Length 129;
Best Local Similarity 83.3%; Pred. No. 8.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
|||||:|
Db 30 TGYYMH 35

Search completed: June 12, 2002, 11:25:35
Job time: 300 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:20:05 ; Search time 49.09 Seconds
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2.985 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	91.9	114	2	US-08-888-366-8	Sequence 8, Appli
2	34	91.9	117	3	US-08-545-809A-90	Sequence 90, Appl
3	34	91.9	123	1	US-08-477-877B-94	Sequence 94, Appl
4	34	91.9	123	2	US-08-472-281A-94	Sequence 94, Appl
5	34	91.9	123	2	US-08-477-989B-94	Sequence 94, Appl
6	34	91.9	124	4	US-09-257-069-2	Sequence 2, Appli
7	34	91.9	243	1	US-08-230-843-4	Sequence 4, Appli
8	34	91.9	243	2	US-08-636-936-4	Sequence 4, Appli
9	32	86.5	288	4	US-09-423-439-38	Sequence 38, Appl
10	32	86.5	445	1	US-08-353-400-33	Sequence 33, Appl
11	32	86.5	464	1	US-08-353-400-36	Sequence 36, Appl
12	32	86.5	585	4	US-09-370-807-4	Sequence 4, Appli
13	32	86.5	611	4	US-09-370-807-2	Sequence 2, Appli
14	32	86.5	673	4	US-09-423-439-32	Sequence 32, Appl
15	31	83.8	116	2	US-08-561-521-41	Sequence 41, Appl
16	31	83.8	116	5	PCT-US95-01219-41	Sequence 41, Appl
17	31	83.8	135	1	US-08-137-117D-27	Sequence 27, Appl
18	31	83.8	135	1	US-08-137-117D-100	Sequence 100, App
19	31	83.8	135	1	US-08-137-117D-102	Sequence 102, App
20	31	83.8	135	1	US-08-137-117D-112	Sequence 112, App
21	31	83.8	135	2	US-08-436-717-27	Sequence 27, Appl
22	31	83.8	135	2	US-08-436-717-100	Sequence 100, App
23	31	83.8	135	2	US-08-436-717-102	Sequence 102, App
24	31	83.8	135	2	US-08-436-717-112	Sequence 112, App
25	30	81.1	275	2	US-08-645-193B-19	Sequence 19, Appl
26	30	81.1	421	4	US-09-239-303-2	Sequence 2, Appli
27	30	81.1	557	2	US-08-793-229-33	Sequence 33, Appl
28	30	81.1	557	3	US-09-285-957-33	Sequence 33, Appl
29	30	81.1	846	1	US-07-731-157A-5	Sequence 5, Appli
30	30	81.1	846	2	US-08-541-780-5	Sequence 5, Appli
31	29	78.4	69	4	US-09-308-003-15	Sequence 15, Appl
32	29	78.4	119	1	US-08-300-386A-65	Sequence 65, Appl
33	29	78.4	119	3	US-08-931-645-65	Sequence 65, Appl
34	29	78.4	119	5	PCT-US95-11235-65	Sequence 65, Appl
35	29	78.4	634	1	US-07-779-049-3	Sequence 3, Appli
36	29	78.4	634	1	US-08-080-240-3	Sequence 3, Appli
37	29	78.4	1025	2	US-08-530-792D-23	Sequence 23, Appl
38	29	78.4	1026	2	US-08-530-792D-22	Sequence 22, Appl
39	29	78.4	2860	2	US-08-826-267-2	Sequence 2, Appli
40	28	75.7	35	2	US-08-765-179B-5	Sequence 5, Appli
41	28	75.7	117	3	US-08-545-809A-128	Sequence 128, App
42	28	75.7	117	4	US-09-157-370-2	Sequence 2, Appli
43	28	75.7	117	4	US-09-025-769B-22	Sequence 22, Appl
44	28	75.7	120	4	US-09-025-769B-36	Sequence 36, Appl
45	28	75.7	120	4	US-09-025-769B-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-08-888-366-8
; Sequence 8, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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;    MOLECULE TYPE:  protein
US-08-888-366-8


  Query Match             91.9%;  Score 34;  DB 2;  Length 114;
  Best Local Similarity   83.3%;  Pred. No. 9.7;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     24 TGYYMH 29


RESULT   2
US-08-545-809A-90
; Sequence 90, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  90:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-545-809A-90


  Query Match             91.9%;  Score 34;  DB 3;  Length 117;
  Best Local Similarity   83.3%;  Pred. No. 9.9;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     49 TGYYMH 54


RESULT   3
US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,877B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polypeptide
;    FEATURE:
;      NAME/KEY:  Human Amu 5-3 heavy chain variable region.
US-08-477-877B-94


  Query Match             91.9%;  Score 34;  DB 1;  Length 123;
  Best Local Similarity   83.3%;  Pred. No. 10;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGYYIH 6
          ||||:|
Db     30 TGYYMH 35


RESULT   4
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:31 ; Search time 136.11 Seconds
(without alignments)
13.873 Million cell updates/sec

Title: US-09-780-035-10
Perfect score: 91
Sequence: 1 GRLNPTTGDANFAEKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	17	22	AAG65300	Anti-IL-18 antibod
2	91	100.0	113	22	AAG65308	Anti-IL-18 antibod
3	91	100.0	113	22	AAG65352	Anti-IL-18 antibod
4	85	93.4	17	22	AAG65306	Anti-IL-18 antibod
5	79	86.8	17	22	AAG65307	Anti-IL-18 antibod
6	63	69.2	123	19	AAW79228	Heavy chain variab
7	58	63.7	115	21	AAB12168	Humanised HBV pre-
8	58	63.7	115	21	AAB12169	Humanised HBV pre-
9	58	63.7	115	21	AAB12172	Humanised HBV pre-
10	58	63.7	118	22	AAU02619	Anti-adipocyte mon
11	58	63.7	123	17	AAR92992	Humanised antibody
12	58	63.7	123	17	AAR92990	Monoclonal antibod
13	56	61.5	123	22	AAU02552	Anti-adipocyte mon
14	55	60.4	117	16	AAR66296	Human immunoglobul
15	55	60.4	120	18	AAW27551	Human Ab heavy cha
16	55	60.4	120	22	AAB49746	Anti-PF4/heparin c
17	55	60.4	128	15	AAR54283	Anti-HIV gp120 imm
18	55	60.4	128	15	AAR54285	Anti-HIV gp120 imm
19	55	60.4	128	15	AAR54286	Anti-HIV gp120 imm
20	55	60.4	128	17	AAW01235	VH region of HIV n
21	55	60.4	128	17	AAW01236	VH region of HIV n
22	55	60.4	128	17	AAW01233	VH region of HIV n
23	55	60.4	128	21	AAY95084	Anti-gp120 antibod
24	55	60.4	128	21	AAY95086	Anti-gp120 antibod
25	55	60.4	128	21	AAY95087	Anti-gp120 antibod
26	55	60.4	128	21	AAY98193	Anti-gp120 antibod
27	55	60.4	128	21	AAY98195	Anti-gp120 antibod
28	55	60.4	128	21	AAY98196	Anti-gp120 antibod
29	55	60.4	146	18	AAW22841	Human anti-tumour
30	55	60.4	156	22	AAB47059	Heavy chain variab
31	55	60.4	245	22	AAB67619	Human leukocyte an
32	55	60.4	249	18	AAW24061	Human WSX receptor
33	54	59.3	105	17	AAR91366	Anti-proenkephalin
34	54	59.3	117	17	AAR88716	Mouse antibody hea
35	54	59.3	118	14	AAR37611	hIL2R Ab H chain V
36	54	59.3	118	14	AAR37609	B-B10 MAb H chain
37	54	59.3	122	21	AAY50959	Human FVIII antibo
38	54	59.3	122	21	AAY50966	Human FVIII antibo
39	54	59.3	127	21	AAY64739	Human 5' EST relat
40	54	59.3	128	15	AAR54288	Anti-HIV gp120 imm
41	54	59.3	128	17	AAW01238	VH region of HIV n
42	54	59.3	128	21	AAY95089	Anti-gp120 antibod
43	54	59.3	128	21	AAY98198	Anti-gp120 antibod
44	53	58.2	98	16	AAR72069	HV1263 VH region.
45	53	58.2	102	18	AAW18841	Human immunoglobul

ALIGNMENTS

RESULT 1
AAG65300
ID AAG65300 standard; protein; 17 AA.
XX
AC AAG65300;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain CDR2 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 25; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain CDR2 fragment.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 91; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLNPTTGDANFAEKFQ 17
||||||||||||||||||
Db 1 grlnpttgdanfaekfq 17

RESULT 2
AAG65308
ID AAG65308 standard; protein; 113 AA.
XX
AC AAG65308;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47511.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain sequence.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 91; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLNPTTGDANFAEKFQ 17
||||||||||||||||||
Db 49 grlnpttgdanfaekfq 65

RESULT 3
AAG65352
ID AAG65352 standard; Protein; 113 AA.
XX
AC AAG65352;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47511.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 86; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 91; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRLNPTTGDANFAEKFQ 17
||||||||||||||||||
Db 49 grlnpttgdanfaekfq 65

RESULT 4
AAG65306
ID AAG65306 standard; protein; 17 AA.
XX
AC AAG65306;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody variable region fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 29; Page 76; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody variable
CC region fragment.
XX
SQ Sequence 17 AA;

Query Match 93.4%; Score 85; DB 22; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.3e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRLNPTTGDANFAEKFQ 17
||||| ||||||||||
Db 1 grlnprtgdanfaekfq 17

RESULT 5
AAG65307
ID AAG65307 standard; protein; 17 AA.
XX
AC AAG65307;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody variable region fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 29; Page 76; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,

```
CC   cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC   agents. The present sequence represents an anti-IL-18 antibody variable
CC   region fragment.
XX
SQ   Sequence   17 AA;


  Query Match             86.8%;  Score 79;  DB 22;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 5.9e-07;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||||| |||| ||||||
Db       1 grlnprtgdaqfaekfq 17


RESULT   6
AAW79228
ID   AAW79228 standard; Protein; 123 AA.
XX
AC   AAW79228;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Heavy chain variable region of human Amu 5-3.
XX
KW   Monoclonal antibody; MAb; LO-CD2a; humanised antibody; chimeric;
KW   T-cell; immune response; CD2 antigen;graft-versus-host disease;
KW   human lymphocyte; transplant rejection; autoimmune disease; Amu 5-3.
XX
OS   Homo sapiens.
XX
PN   US5817311-A.
XX
PD   06-OCT-1998.
XX
PF   07-JUN-1995;   95US-0472281.
XX
PR   07-JUN-1995;   95US-0472281.
PR   05-MAR-1993;   93US-0027008.
PR   09-SEP-1993;   93US-0119032.
PR   29-MAR-1995;   95US-0407009.
XX
PA   (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI   Bazin H,  Latinne D;
XX
DR   WPI; 1998-556337/47.
XX
PT   Inhibition of T-cell mediated immune response with anti-CD2
PT   monoclonal antibody LO-CD2a - used for preventing transplant
PT   rejection or for treating graft-versus-host disease or auto-immune
PT   diseases
XX
PS   Example 7; Fig 33; 96pp; English.
XX
CC   This represents the amino acid sequence of the light chain variable
CC   region of human antibody clone Amu 5-3. This is used to consruct a
CC   humanised antibody LO-CD2a. The invention relates to the use of the
CC   monoclonal antibody (MAb) LO-CD2a or a humanised or a chimeric version
CC   of the LO-CD2a antibody for the inhibition of a T-cell mediated immune
CC   response in a patient. The MAb LO-CD2a (produced by hybridoma cell line
CC   ATCC HB 11423) can bind to an epitope on the CD2 antigen of the human
CC   lymphocytes. The T-cell mediated immune response in a patient can be
CC   inhibited by administering the MAb LO-CD2a or an antibody that binds to
CC   the same human lymphocyte epitope as LO-CD2a. The method is used for
CC   preventing transplant rejection or for treating graft-versus-host
CC   disease or for treating autoimmune diseases.
XX
SQ   Sequence   123 AA;

  Query Match             69.2%;  Score 63;  DB 19;  Length 123;
  Best Local Similarity   58.8%;  Pred. No. 0.0031;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      49 grinpnsggtnyaqkfq 65


RESULT   7
AAB12168
ID   AAB12168 standard; Protein; 115 AA.
XX
AC   AAB12168;
XX
DT   17-JAN-2001  (first entry)
XX
DE   Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.
XX
KW   Humanised antibody; HBV surface antigen pre-S1; mouse;
KW   human; hepatitis B; liver cirrhosis; liver cancer.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
XX
PN   WO200031141-A1.
XX
PD   02-JUN-2000.
XX
PF   19-NOV-1999;   99WO-KR00699.
XX
PR   19-NOV-1998;   98KR-0049663.
XX
PA   (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
PA   (GREC ) KOREA GREEN CROSS CORP.
XX
PI   Hong HJ,  Ryu CJ,  Hur H;
XX
DR   WPI; 2000-400048/34.
DR   N-PSDB; AAA62118.
XX
PT   Humanized antibody specific for hepatitis B virus surface antigen
PT   pre-S1, containing humanized heavy and light chain regions, useful for
PT   preventing hepatitis B virus (HBV) infection and for treating chronic
PT   hepatitis B -
XX
PS   Claim 2; Fig 1; 61pp; English.
XX
CC   Hepatitis B virus (HBV) is responsible for hepatitis infection in
CC   humans, which may progress to liver cirrhosis or cancer. One of HBV's
CC   surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
CC   antigen may efficiently neutralise HBV. The present invention relates to
CC   humanised antibodies specific for HBV surface antigen pre-S1. The
CC   humanised antibodies are useful for preventing HBV infection and for
CC   treating chronic hepatitis B. The Complementarity Determining Regions of
CC   mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
CC   the humanised antibodies of the present invention. The present sequence
CC   is the humanised pre-S1 antibody HKR127HC(I) heavy chain variable region
CC   (VH). The coding sequence for the present sequence was produced from the
CC   coding sequence of the mouse pre-S1 antibody VH sequence (AAA62115).
XX
SQ   Sequence   115 AA;


  Query Match             63.7%;  Score 58;  DB 21;  Length 115;
  Best Local Similarity   58.8%;  Pred. No. 0.022;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||: |  || |:|:|||
Db      49 griypgdgdtnyaqkfq 65


RESULT   8
```

```
AAB12169
ID   AAB12169 standard; Protein; 115 AA.
XX
AC   AAB12169;
XX
DT   17-JAN-2001  (first entry)
XX
DE   Humanised HBV pre-S1 antibody HKR127HC(III) heavy chain variable region.
XX
KW   Humanised antibody; HBV surface antigen pre-S1; mouse;
KW   human; hepatitis B; liver cirrhosis; liver cancer.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
XX
PN   WO200031141-A1.
XX
PD   02-JUN-2000.
XX
PF   19-NOV-1999;   99WO-KR00699.
XX
PR   19-NOV-1998;   98KR-0049663.
XX
PA   (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
PA   (GREC ) KOREA GREEN CROSS CORP.
XX
PI   Hong HJ,  Ryu CJ,  Hur H;
XX
DR   WPI; 2000-400048/34.
DR   N-PSDB; AAA62119.
XX
PT   Humanized antibody specific for hepatitis B virus surface antigen
PT   pre-S1, containing humanized heavy and light chain regions, useful for
PT   preventing hepatitis B virus (HBV) infection and for treating chronic
PT   hepatitis B -
XX
PS   Claim 3; Fig 1; 61pp; English.
XX
CC   Hepatitis B virus (HBV) is responsible for hepatitis infection in
CC   humans, which may progress to liver cirrhosis or cancer. One of HBV's
CC   surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
CC   antigen may efficiently neutralise HBV. The present invention relates to
CC   humanised antibodies specific for HBV surface antigen pre-S1. The
CC   humanised antibodies are useful for preventing HBV infection and for
CC   treating chronic hepatitis B. The Complementarity Determining Regions of
CC   mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
CC   the humanised antibodies of the present invention. The present sequence
CC   is the humanised pre-S1 antibody HKR127HC(III) heavy chain variable
CC   region (VH). The coding sequence for the present sequence was produced
CC   from the coding sequence of the mouse pre-S1 antibody VH sequence
CC   (AAA62115).
XX
SQ   Sequence   115 AA;

  Query Match             63.7%;  Score 58;  DB 21;  Length 115;
  Best Local Similarity   58.8%;  Pred. No. 0.022;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||: |  || |:|:|||
Db      49 griypgdgdtnyaqkfq 65


RESULT   9
AAB12172
ID   AAB12172 standard; Protein; 115 AA.
XX
AC   AAB12172;
XX
DT   17-JAN-2001  (first entry)
XX
DE   Humanised HBV pre-S1 antibody HKR127HC(II) heavy chain variable region.
XX
KW   Humanised antibody; HBV surface antigen pre-S1; mouse;
KW   human; hepatitis B; liver cirrhosis; liver cancer.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
XX
PN   WO200031141-A1.
XX
PD   02-JUN-2000.
XX
PF   19-NOV-1999;   99WO-KR00699.
XX
PR   19-NOV-1998;   98KR-0049663.
XX
PA   (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
PA   (GREC ) KOREA GREEN CROSS CORP.
XX
PI   Hong HJ,  Ryu CJ,  Hur H;
XX
DR   WPI; 2000-400048/34.
DR   N-PSDB; AAA62117.
XX
PT   Humanized antibody specific for hepatitis B virus surface antigen
PT   pre-S1, containing humanized heavy and light chain regions, useful for
PT   preventing hepatitis B virus (HBV) infection and for treating chronic
PT   hepatitis B -
XX
PS   Disclosure; Fig 1; 61pp; English.
XX
CC   Hepatitis B virus (HBV) is responsible for hepatitis infection in
CC   humans, which may progress to liver cirrhosis or cancer. One of HBV's
CC   surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
CC   antigen may efficiently neutralise HBV. The present invention relates to
CC   humanised antibodies specific for HBV surface antigen pre-S1. The
CC   humanised antibodies are useful for preventing HBV infection and for
CC   treating chronic hepatitis B. The Complementarity Determining Regions of
CC   mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
CC   the humanised antibodies of the present invention. The present sequence
CC   is the humanised pre-S1 antibody HKR127HC(II) heavy chain variable
CC   region (VH). The coding sequence for the present sequence was produced
CC   from the coding sequence of the mouse pre-S1 antibody (AAA62115).
XX
SQ   Sequence   115 AA;

  Query Match             63.7%;  Score 58;  DB 21;  Length 115;
  Best Local Similarity   58.8%;  Pred. No. 0.022;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||: |  || |:|:|||
Db      49 griypgdgdtnyaqkfq 65


RESULT  10
AAU02619
ID   AAU02619 standard; Protein; 118 AA.
XX
AC   AAU02619;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Anti-adipocyte monoclonal antibody heavy chain, FAT 106.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW   heart disease; complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO200127279-A1.
XX
PD   19-APR-2001.
```

```
XX
PF   11-OCT-2000; 2000WO-GB03900.
XX
PR   12-OCT-1999;   99US-0158812.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM,  Main SH,  Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   N-PSDB; AAS03519.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity
PT   related diseases -
XX
PS   Claim 1; Page 167; 182pp; English.
XX
CC   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC   sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC   chain, and heavy chain complementarity determining regions (CDR) of the
CC   invention. The antibodies can be used in the treatment of obesity and
CC   obesity related diseases. The antibodies can be used to deliver drugs or
CC   pro-drugs directly to the fat mass of an obese patient or the antibody
CC   can be used as a therapeutic itself. Antibodies binding specifically to
CC   adipocytes can be used to activate the immune system to destroy the cells
CC   by complement mediated lysis. The antibodies may be labeled with a
CC   detectable label such as radiolabel, fluorescent or chemical group and
CC   used in methods of diagnosis in human subjects e.g. to determine the
CC   presence of adipocyte antigen on the surface of an adipocyte to detect or
CC   determine the presence or level of adipocytes in a cell or tissue sample.
CC   The antibodies can be used as an alternative means of treatment for obese
CC   patients other than undergoing surgery to remove excess fat. Antibodies
CC   for different types of fat deposits can also be produced e.g. intra-
CC   abdominal fat associated with heart disease.
XX
SQ   Sequence   118 AA;


  Query Match             63.7%;  Score 58;  DB 22;  Length 118;
  Best Local Similarity   58.8%;  Pred. No. 0.022;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :|  |:|||||
Db      49 gwinpnsggtnyaekfq 65


RESULT  11
AAR92992
ID   AAR92992 standard; Protein; 123 AA.
XX
AC   AAR92992;
XX
DT   18-MAY-1996  (first entry)
XX
DE   Humanised antibody IOR-R3 variable region heavy chain.
XX
KW   Humanised antibody; IOR-R3; monoclonal antibody; mouse; heavy chain;
KW   variable region; epidermal growth factor receptor; hybridoma;
KW   framework; cloning; computer; algorithm; human; immunogenicity;
KW   site-directed mutagenesis; T-lymphocyte epitope;
KW   complementarity determining region; tertiary structure; point mutation;
KW   antibody engineering; protein engineering; antitumour; cancer; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 11..12
FT                   /note= "Mutated amino acids"
FT   Region          26..30
FT                   /note= "Amino acids involved in tertiary structure"
FT   Region          31..35
FT                   /note= "Complementarity determining region"
FT   Region          34
FT                   /note= "Amino acid involved in tertiary structure"
FT   Region          50..66
FT                   /note= "Complementarity determining region"
FT   Region          53..56
FT                   /note= "Amino acids involved in tertiary structure"
FT   Region          72
FT                   /note= "Amino acid involved in tertiary structure"
FT   Misc-difference 76..77
FT                   /note= "Mutated amino acids"
FT   Misc-difference 79
FT                   /note= "Mutated amino acid"
FT   Misc-difference 87
FT                   /note= "Mutated amino acid"
FT   Region          98
FT                   /note= "Amino acid involved in tertiary structure"
FT   Region          99..108
FT                   /note= "Complementarity determining region"
XX
PN   EP699755-A2.
XX
PD   06-MAR-1996.
XX
PF   27-JUN-1995;   95EP-0201752.
XX
PR   30-JUN-1994;   94CU-0000080.
XX
PA   (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI   Mateo de Acosta del Rio CM,  Rodriguez RP,  Valladares JL;
XX
DR   WPI; 1996-130770/14.
XX
PT   Identifying interspecies differences in amino acid sequence of Ig
PT   T-cell epitopes - by sequence comparison, also humanised antibodies
PT   contg. altered T-cell epitopes, retaining antigen specificity but
PT   not immunogenicity, esp. for tumour treatment
XX
PS   Claim 14; Fig 2; 33pp; English.
XX
CC   The sequence represents a humanised mutant form of a heavy chain
CC   variable region from monoclonal antibody IOR-R3, specific for
CC   epidermal growth factor receptor and originally isolated from a
CC   mouse hybridoma.  The native antibody framework sequence (AAR92990) is
CC   analysed for T-cell antigenic sequences using a computer algorithm,
CC   and compared with human Ig sequences.  The human Ig with highest
CC   homology (e.g. AAR92991) is isolated, and residues not within a
CC   complementarity determining region, canonical structure or Vernier
CC   zone are modified to reduce immunogenicity in humans to produce a
CC   humanised antibody.  This method, which involves the introduction of
CC   only a few point mutations into T-cell epitope coding regions, is
CC   generally applicable in humanisation of mouse antibodies.  The
CC   resulting humanised antibodies may be used e.g. as antitumour agents.
CC   They retain the antigen recognition of the original antibody, but are
CC   not immunogenic in humans.
XX
SQ   Sequence   123 AA;


  Query Match             63.7%;  Score 58;  DB 17;  Length 123;
  Best Local Similarity   58.8%;  Pred. No. 0.023;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|||:| :|| |||:
Db      49 gginptsggsnfnekfk 65


RESULT  12
AAR92990
ID   AAR92990 standard; Protein; 123 AA.
XX
```

AC AAR92990;
XX
DT 18-MAY-1996 (first entry)
XX
DE Monoclonal antibody IOR-R3 variable region heavy chain.
XX
KW IOR-R3; monoclonal antibody; mouse; heavy chain; variable region;
KW epidermal growth factor receptor; hybridoma; framework; cloning;
KW computer; algorithm; human; immunogenicity; site-directed mutagenesis;
KW T-lymphocyte epitope; complementarity determining region;
KW tertiary structure; point mutation; antibody engineering;
KW protein engineering; humanised antibody; antitumour; cancer;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 3..14
FT /note= "Predicted T-lymphocyte antigen"
FT Region 26..30
FT /note= "Amino acids involved in tertiary structure"
FT Region 31..35
FT /note= "Complementarity determining region"
FT Region 34
FT /note= "Amino acid involved in tertiary structure"
FT Region 39..56
FT /note= "Predicted T-lymphocyte antigen"
FT Region 50..66
FT /note= "Complementarity determining region"
FT Region 53..56
FT /note= "Amino acids involved in tertiary structure"
FT Region 72
FT /note= "Amino acid involved in tertiary structure"
FT Region 75..88
FT /note= "Predicted T-lymphocyte antigen"
FT Region 98
FT /note= "Amino acid involved in tertiary structure"
FT Region 99..108
FT /note= "Complementarity determining region"
FT Region 103..116
FT /note= "Predicted T-lymphocyte antigen"
XX
PN EP699755-A2.
XX
PD 06-MAR-1996.
XX
PF 27-JUN-1995; 95EP-0201752.
XX
PR 30-JUN-1994; 94CU-0000080.
XX
PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI Mateo de Acosta del Rio CM, Rodriguez RP, Valladares JL;
XX
DR WPI; 1996-130770/14.
XX
PT Identifying interspecies differences in amino acid sequence of Ig
PT T-cell epitopes - by sequence comparison, also humanised antibodies
PT contg. altered T-cell epitopes, retaining antigen specificity but
PT not immunogenicity, esp. for tumour treatment
XX
PS Claim 14; Fig 2; 33pp; English.
XX
CC The sequence represents the heavy chain variable region from
CC monoclonal antibody IOR-R3, specific for epidermal growth factor
CC receptor, produced by a mouse hybridoma. The framework sequence is
CC analysed for T-cell antigenic sequences using a computer algorithm,
CC and compared with human Ig sequences. The human Ig with highest
CC homology (AAR92991) is isolated, and residues not within a
CC complementarity determining region, canonical structure or Vernier
CC zone are modified to reduce immunogenicity in humans (e.g. in
CC sequence AAR92992). This method, which involves the introduction of
CC only a few point mutations into T-cell epitope coding regions, is
CC generally applicable in humanisation of mouse antibodies. The
CC resulting humanised antibodies may be used e.g. as antitumour agents.
CC They retain the antigen recognition of the original antibody, but are
CC not immunogenic in humans.
XX
SQ Sequence 123 AA;

Query Match 63.7%; Score 58; DB 17; Length 123;
Best Local Similarity 58.8%; Pred. No. 0.023;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GRLNPTTGDANFAEKFQ 17
| :|||:| :|| |||:
Db 49 gginptsggsnfnekfk 65

RESULT 13
AAU02552
ID AAU02552 standard; Protein; 123 AA.
XX
AC AAU02552;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody heavy chain, FAT 38.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03452.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS Claim 1; Page 124-125; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 123 AA;

```
  Query Match             61.5%;  Score 56;  DB 22;  Length 123;
  Best Local Similarity   52.9%;  Pred. No. 0.052;
  Matches    9;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :||  :|:|||
Db      49 gwmnpnsgdtgyaqkfq 65


RESULT  14
AAR66296
ID   AAR66296 standard; Protein; 117 AA.
XX
AC   AAR66296;
XX
DT   07-AUG-1995  (first entry)
XX
DE   Human immunoglobulin variable heavy chain #2.
XX
KW   Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW   cosmid; placenta; vector; pJB81; E.coli; mammalian.
XX
OS   Homo sapiens.
XX
PN   WO9426895-A.
XX
PD   24-NOV-1994.
XX
PF   10-MAY-1993;   93WO-JP00603.
XX
PR   10-MAY-1993;   93WO-JP00603.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Honjo T,  Matsuda F;
XX
DR   WPI; 1995-006791/01.
DR   N-PSDB; AAQ78940.
XX
PT   DNA fragment comprising human immunoglobulin Vh genes - for the
PT   production of human immunoglobulin in mammalian hosts
XX
PS   Disclosure; Page 32-33; 130pp; Japanese.
XX
CC   Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
CC   chain sequences encoded by novel isolated genes.  The genes
CC   (AAQ78939-79002) were isolated and cloned from a series of cosmid
CC   constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR
CC   amplification using primers AAQ78917-38.  The genes are subdivided into 5
CC   families of Vh genes.  The fragments cover a region of 800 kb.  The DNA
CC   fragments were isolated from high molecular weight DNA from human
CC   placenta.  The DNA was partially digested with TaqI restriction enzyme.
CC   The fragments were separated by gel elecrophoresis and 35-45 kb fractions
CC   were collected.  The fragments were ligated with ClaI-digested cosmid
CC   vector pJB81.  The ligation products were in vitro packed and infected
CC   into E.coli 490A.  The fragments were then subcloned by colony
CC   hybridisation.  The Vh genes and the DNA fragments encoding them are
CC   useful in producing human immunoglobulin in mammalian hosts.
XX
SQ   Sequence   117 AA;


  Query Match             60.4%;  Score 55;  DB 16;  Length 117;
  Best Local Similarity   52.9%;  Pred. No. 0.074;
  Matches    9;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :|  |:|:|||
Db      68 gwinpnsggtnyaqkfq 84


RESULT  15
AAW27551
ID   AAW27551 standard; Protein; 120 AA.
XX
AC   AAW27551;
XX
DT   23-JAN-1998  (first entry)
XX
DE   Human Ab heavy chain variable region VH1B consensus.
XX
KW   Human; antibody; preparation; library; VH1B; variable region;
KW   heavy chain; consensus.
XX
OS   Homo sapiens.
XX
PN   WO9708320-A1.
XX
PD   06-MAR-1997.
XX
PF   19-AUG-1996;   96WO-EP03647.
XX
PR   18-AUG-1995;   95EP-0113021.
XX
PA   (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX
PI   Ge L,  Ilag V,  Knappik A,  Moroney S,  Pack P,  Plueckthun A;
XX
DR   WPI; 1997-179277/16.
DR   N-PSDB; AAT87949.
XX
PT   Preparation of human derived antibody gene library - using synthetic
PT   consensus sequences, and signal consensus antibody gene as universal
PT   framework for highly diverse antibody libraries
XX
PS   Example 1; Fig 5B; 436pp; English.
XX
CC   The present sequence is the human antibody heavy chain
CC   variable region synthetic sequence VH1B, used in the preparation of
CC   a human derived antibody gene library.
XX
SQ   Sequence   120 AA;


  Query Match             60.4%;  Score 55;  DB 18;  Length 120;
  Best Local Similarity   52.9%;  Pred. No. 0.076;
  Matches    9;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :|  |:|:|||
Db      49 gwinpnsggtnyaqkfq 65


Search completed: June 12, 2002, 11:23:32
Job time: 317 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:25:35 ; Search time 61.61 Seconds
(without alignments)
26.514 Million cell updates/sec

Title: US-09-780-035-10
Perfect score: 91
Sequence: 1 GRLNPTTGDANFAEKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	69.2	98	2	S26910	Ig heavy chain V r
2	63	69.2	117	1	HVHU35	Ig heavy chain pre
3	58	63.7	104	2	S69899	Ig heavy chain V r
4	58	63.7	123	2	D33548	Ig heavy chain V-1
5	57	62.6	288	2	S29690	Ig heavy chain VDJ
6	55	60.4	98	2	PH1123	Ig heavy chain V r
7	55	60.4	98	2	S26938	Ig heavy chain V r
8	55	60.4	98	2	S26912	Ig heavy chain V r
9	55	60.4	110	2	PH1669	Ig heavy chain V r
10	55	60.4	117	2	S31680	Ig heavy chain V r
11	55	60.4	117	2	S18551	Ig heavy chain V r
12	55	60.4	118	2	S36265	Ig heavy chain V r
13	55	60.4	129	2	S46393	Ig heavy chain V r
14	55	60.4	135	2	S49530	anti-Sm antibody V
15	54	59.3	77	2	S46467	Ig heavy chain V r
16	54	59.3	101	2	S26314	Ig heavy chain V r
17	54	59.3	116	2	S55542	Ig heavy chain V r
18	53	58.2	97	2	PH0870	Ig heavy chain V r
19	53	58.2	98	2	S46463	Ig heavy chain V1
20	53	58.2	109	2	PH1671	Ig heavy chain V r
21	51	56.0	98	2	PH1157	Ig heavy chain V r
22	51	56.0	98	2	I28833	Ig kappa chain V r
23	51	56.0	98	2	S26918	Ig heavy chain V r
24	51	56.0	108	2	PH0985	Ig heavy chain V r
25	51	56.0	132	2	S31596	Ig heavy chain V r
26	51	56.0	136	2	S31600	Ig heavy chain V r
27	50	54.9	107	2	PH1013	Ig heavy chain V r
28	50	54.9	108	2	PH1012	Ig heavy chain V r
29	50	54.9	131	2	A27472	Ig heavy chain pre
30	49	53.8	67	2	PH1146	Ig heavy chain V r
31	49	53.8	85	2	E37262	Ig heavy chain V r
32	49	53.8	97	2	PH1155	Ig heavy chain V r
33	49	53.8	98	2	PH1112	Ig heavy chain V r
34	49	53.8	98	2	S26920	Ig heavy chain V r
35	49	53.8	117	1	HVHUHG	Ig heavy chain pre
36	49	53.8	120	1	MHMS15	Ig heavy chain V r
37	49	53.8	136	2	PL0208	Ig heavy chain pre
38	49	53.8	138	1	HVMST7	Ig heavy chain pre
39	49	53.8	143	1	E1HUND	Ig heavy chain pre
40	48	52.7	56	2	PH1158	Ig heavy chain V r
41	48	52.7	86	2	S29544	Ig heavy chain V r
42	48	52.7	97	2	S16028	Ig heavy chain V r
43	48	52.7	98	2	S17604	Ig heavy chain V r
44	48	52.7	98	2	S26921	Ig heavy chain V r
45	48	52.7	109	2	PH0973	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S26910
Ig heavy chain V region (DP-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S26910
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117
A;Accession: S26910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12303; NID:g32847; PIDN:CAA78173.1; PID:g32848
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 63; DB 2; Length 98;
Best Local Similarity 58.8%; Pred. No. 0.0014;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      49 GRINPNSGGTNYAQKFQ 65
```

RESULT 2
HVHU35
Ig heavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: S00476; S34013
R;Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fuk
EMBO J. 7, 1047-1051, 1988
A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain
A;Reference number: S00476; MUID:88296408
A;Accession: S00476
A;Molecule type: DNA
A;Residues: 1-117 <MATS>
A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Note: the authors translated the codon AGT for residue 89 as Met
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclon
A;Reference number: S34001; MUID:93209281
A;Accession: S34013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 20-116 <MAR>

C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 63; DB 1; Length 117;
Best Local Similarity 58.8%; Pred. No. 0.0017;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      68 GRINPNSGGTNYAQKFQ 84
```

RESULT 3
S69899
Ig heavy chain V region (clone RFTS7H), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69899
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respo
A;Reference number: S69896; MUID:93272805
A;Accession: S69899
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-104 <RAN>
A;Cross-references: EMBL:Z34893; NID:g509803; PIDN:CAA84376.1; PID:g509804
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 63.7%; Score 58; DB 2; Length 104;
Best Local Similarity 52.9%; Pred. No. 0.011;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  ::|:|||
Db      49 GRINPNSGGTHYAQKFQ 65
```

RESULT 4
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 63.7%; Score 58; DB 2; Length 123;
Best Local Similarity 58.8%; Pred. No. 0.013;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :|  |:|||||
Db      49 GWINPNSGGTNYAEKFQ 65
```

RESULT 5
S29690
Ig heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DAM>
A;Cross-references: EMBL:X68782; NID:g56442; PID:g1334294
A;Experimental source: strain DZB
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 62.6%; Score 57; DB 2; Length 288;
Best Local Similarity 52.9%; Pred. No. 0.05;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:||  |:  :||||:
Db      46 GRINPANGNTEYAEKFK 62
```

RESULT 6
PH1123
Ig heavy chain V region (clone V2059.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1123
R;Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A;Reference number: PH1105; MUID:92364545
A;Accession: PH1123
A;Molecule type: DNA
A;Residues: 1-98 <SCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 55; DB 2; Length 98;
Best Local Similarity 52.9%; Pred. No. 0.034;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GRLNPTTGDANFAEKFQ 17
           ||::| :| ||: |||:
Db      49 GRIDPNSGGANYNEKFK 65
```

RESULT 7
S26938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A;Reference number: S26885; MUID:93021117
A;Accession: S26938
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:39:12 ; Search time 29.47 Seconds
(without alignments)
22.336 Million cell updates/sec

Title: US-09-780-035-10
Perfect score: 91
Sequence: 1 GRLNPTTGDANFAEKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	69.2	117	1	HV1G_HUMAN	P23083 homo sapien
2	49	53.8	117	1	HV1B_HUMAN	P01743 homo sapien
3	49	53.8	120	1	HV50_MOUSE	P06329 mus musculu
4	49	53.8	138	1	HV48_MOUSE	P03980 mus musculu
5	49	53.8	147	1	HV1C_HUMAN	P01744 homo sapien
6	48	52.7	117	1	HV04_MOUSE	P01748 mus musculu
7	48	52.7	117	1	HV06_MOUSE	P01750 mus musculu
8	45	49.5	117	1	HV09_MOUSE	P01753 mus musculu
9	45	49.5	117	1	HV10_MOUSE	P01754 mus musculu
10	45	49.5	139	1	HV07_MOUSE	P01751 mus musculu
11	44	48.4	324	1	MCH_METOR	Q9rpw7 methylobact
12	43	47.3	140	1	HV02_MOUSE	P01746 mus musculu
13	42	46.2	117	1	HV1A_HUMAN	P01742 homo sapien
14	42	46.2	171	1	RPB7_YEAST	P34087 saccharomyc
15	41	45.1	182	1	Y033_NPVAC	P21286 autographa
16	41	45.1	340	1	Y269_MYCGE	Q49407 mycoplasma
17	41	45.1	426	1	FIBP_ADE04	P36844 human adeno
18	40	44.0	117	1	HV12_MOUSE	P01756 mus musculu
19	40	44.0	117	1	HV13_MOUSE	P01757 mus musculu
20	40	44.0	117	1	HV49_MOUSE	P06328 mus musculu
21	40	44.0	118	1	HV51_MOUSE	P06330 mus musculu
22	40	44.0	233	1	FLPA_AERPE	Q9y9u3 aeropyrum p
23	39	42.9	137	1	HV11_MOUSE	P01755 mus musculu
24	39	42.9	445	1	TIG_RICPR	Q9zcb7 rickettsia
25	39	42.9	548	1	VG31_BPML5	Q05240 mycobacteri
26	39	42.9	735	1	CATA_BACST	P14412 bacillus st
27	39	42.9	750	1	HEPA_HSV11	P10192 herpes simp
28	39	42.9	779	1	K6PF_RAT	P47858 rattus norv
29	39	42.9	804	1	FPS_DROME	P18106 drosophila
30	39	42.9	1011	1	HDA9_HUMAN	Q9ukv0 homo sapien
31	38.5	42.3	767	1	MAO2_RICPR	Q9zdf6 rickettsia
32	38	41.8	120	1	HV03_MOUSE	P01747 mus musculu
33	38	41.8	255	1	RL8A_YEAST	P17076 saccharomyc
34	38	41.8	255	1	RL8B_YEAST	P29453 saccharomyc
35	38	41.8	545	1	CHLN_CHLRE	P29683 chlamydomon
36	38	41.8	556	1	Y281_MYCGE	P47523 mycoplasma
37	38	41.8	1257	1	CAML_HUMAN	P32004 homo sapien
38	38	41.8	2184	1	RRPL_CDVO	P24658 canine dist
39	37	40.7	115	1	RA2B_ARATH	P51407 arabidopsis
40	37	40.7	135	1	RS9_PYRAB	Q9v195 pyrococcus
41	37	40.7	135	1	RS9_PYRHO	O59299 pyrococcus
42	37	40.7	186	1	BPHE_COMTE	Q46373 comamonas t
43	37	40.7	249	1	UPPS_SYNY3	Q55482 synechocyst
44	37	40.7	299	1	JAM1_HUMAN	Q9y624 homo sapien
45	37	40.7	339	1	YTH6_RHOER	P43484 rhodococcus

ALIGNMENTS

```
RESULT   1
HV1G_HUMAN
ID   HV1G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V-I REGION V35.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13009 MW;  BE61CE63F8CE97BD CRC64;


  Query Match             69.2%;  Score 63;  DB 1;  Length 117;
  Best Local Similarity   58.8%;  Pred. No. 0.00071;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      68 GRINPNSGGTNYAQKFQ 84


RESULT   2
HV1B_HUMAN
ID   HV1B_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
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```
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION HG3.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12946 MW;  2D3F92FC60CD1FE7 CRC64;


  Query Match             53.8%;  Score 49;  DB 1;  Length 117;
  Best Local Similarity   47.1%;  Pred. No. 0.18;
  Matches    8;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 GRLNPTTGDANFAEKFQ 17
          | :||: |  ::|:|||
Db     68 GIINPSGGSTSYAQKFQ 84


RESULT   3
HV50_MOUSE
ID   HV50_MOUSE     STANDARD;      PRT;   120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MHMS15.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN       1     98       V SEGMENT.
FT   DOMAIN      99    105       D SEGMENT.
FT   DOMAIN     106    120       J SEGMENT.
FT   DISULFID    22     96       BY SIMILARITY.
FT   NON_TER    120    120
SQ   SEQUENCE   120 AA;  13311 MW;  914453F426F09834 CRC64;


  Query Match             53.8%;  Score 49;  DB 1;  Length 120;
  Best Local Similarity   47.1%;  Pred. No. 0.18;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 GRLNPTTGDANFAEKFQ 17
          | :||: |  |: |||:
Db     49 GGINPSNGGTNYNEKFK 65


RESULT   4
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN      21     49       FRAMEWORK-1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      55     68       FRAMEWORK-2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      86    117       FRAMEWORK-3.
FT   DOMAIN     118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     128    138       FRAMEWORK-4.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;


  Query Match             53.8%;  Score 49;  DB 1;  Length 138;
  Best Local Similarity   47.1%;  Pred. No. 0.21;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 GRLNPTTGDANFAEKFQ 17
          | :||  | :|: |||:
Db     68 GEINPNDGRSNYNEKFK 84


RESULT   5
HV1C_HUMAN
ID   HV1C_HUMAN     STANDARD;      PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:38:37 ; Search time 107.96 Seconds
(without alignments)
27.241 Million cell updates/sec

Title: US-09-780-035-10
Perfect score: 91
Sequence: 1 GRLNPTTGDANFAEKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	58.2	116	4	Q9UL89	Q9ul89 homo sapien
2	51	56.0	140	11	Q924P8	Q924p8 mus musculu
3	51	56.0	142	11	Q924Q1	Q924q1 mus musculu
4	51	56.0	278	11	Q921K1	Q921k1 mus musculu
5	49	53.8	124	4	Q9UL92	Q9ul92 homo sapien
6	49	53.8	159	4	Q96QS0	Q96qs0 homo sapien
7	48	52.7	109	11	Q9JL85	Q9jl85 mus musculu
8	48	52.7	125	4	Q9UL95	Q9ul95 homo sapien
9	48	52.7	614	4	Q96GA6	Q96ga6 homo sapien
10	47	51.6	119	4	Q9UL94	Q9ul94 homo sapien
11	46	50.5	110	11	Q9JL77	Q9jl77 mus musculu
12	46	50.5	499	16	Q9WZI5	Q9wzi5 thermotoga
13	45	49.5	137	11	Q924R6	Q924r6 mus musculu
14	45	49.5	139	11	Q924R5	Q924r5 mus musculu
15	45	49.5	140	11	Q924R2	Q924r2 mus musculu
16	45	49.5	141	11	Q924Q4	Q924q4 mus musculu
17	45	49.5	143	11	Q924R7	Q924r7 mus musculu
18	45	49.5	143	11	Q924R0	Q924r0 mus musculu
19	45	49.5	143	11	Q924Q5	Q924q5 mus musculu
20	45	49.5	143	11	Q91VA2	Q91va2 mus musculu
21	45	49.5	144	11	Q924P5	Q924p5 mus musculu
22	45	49.5	145	11	Q924R4	Q924r4 mus musculu
23	45	49.5	145	11	Q924R3	Q924r3 mus musculu
24	45	49.5	145	11	Q924R1	Q924r1 mus musculu
25	45	49.5	145	11	Q924Q9	Q924q9 mus musculu
26	45	49.5	145	11	Q924Q7	Q924q7 mus musculu
27	45	49.5	145	11	Q924Q6	Q924q6 mus musculu
28	45	49.5	145	11	Q924P7	Q924p7 mus musculu
29	45	49.5	146	11	Q924R8	Q924r8 mus musculu
30	45	49.5	146	11	Q924Q8	Q924q8 mus musculu
31	45	49.5	146	11	Q924Q3	Q924q3 mus musculu
32	44	48.4	111	11	Q9D9B8	Q9d9b8 mus musculu
33	44	48.4	215	3	Q96W27	Q96w27 galerina se
34	44	48.4	522	4	Q92573	Q92573 homo sapien
35	44	48.4	649	11	Q9D296	Q9d296 mus musculu
36	44	48.4	692	11	Q99MI9	Q99mi9 cricetulus
37	44	48.4	692	11	Q922X9	Q922x9 mus musculu
38	44	48.4	729	11	Q99MJ0	Q99mj0 cricetulus
39	43	47.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
40	43	47.3	517	5	Q9XTC2	Q9xtc2 caenorhabdi
41	43	47.3	1235	5	Q9VYF3	Q9vyf3 drosophila
42	42.5	46.7	196	3	O74221	O74221 podospora a
43	42	46.2	151	2	Q9ANS4	Q9ans4 rhodobacter
44	42	46.2	173	3	Q9C474	Q9c474 candida alb
45	42	46.2	258	2	Q93N39	Q93n39 coxiella bu

ALIGNMENTS

RESULT 1
Q9UL89
ID Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 58.2%; Score 53; DB 4; Length 116;
Best Local Similarity 58.8%; Pred. No. 0.3;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 GRLNPTTGDANFAEKFQ 17
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Db     45 GRIIPILGIANYAQKFQ 61
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RESULT   2
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ID   Q924P8      PRELIMINARY;      PRT;   140 AA.
AC   Q924P8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   V23-D-J-C MU PROTEIN (FRAGMENT).
GN   V23-D-J-C MU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069917; BAB63933.1; -.
FT   NON_TER       1      1
FT   NON_TER     140    140
SQ   SEQUENCE   140 AA;  15392 MW;  904C80C82548C936 CRC64;


  Query Match             56.0%;  Score 51;  DB 11;  Length 140;
  Best Local Similarity   47.1%;  Pred. No. 0.78;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :||: |  |: |||:
Db      49 GNINPSNGGTNYNEKFK 65


RESULT   3
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ID   Q924Q1      PRELIMINARY;      PRT;   142 AA.
AC   Q924Q1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   V23-D-J-C MU PROTEIN (FRAGMENT).
GN   V23-D-J-C MU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069913; BAB63929.1; -.
FT   NON_TER       1      1
FT   NON_TER     142    142
SQ   SEQUENCE   142 AA;  15622 MW;  24A265CE4EA4318B CRC64;


  Query Match             56.0%;  Score 51;  DB 11;  Length 142;
  Best Local Similarity   47.1%;  Pred. No. 0.79;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :||: |  |: |||:
Db      49 GNINPSNGGTNYNEKFK 65


RESULT   4
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ID   Q921K1      PRELIMINARY;      PRT;   278 AA.
AC   Q921K1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:18977).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012207; AAH12207.1; -.
SQ   SEQUENCE   278 AA;  29778 MW;  F894F955DDCD948A CRC64;


  Query Match             56.0%;  Score 51;  DB 11;  Length 278;
  Best Local Similarity   47.1%;  Pred. No. 1.6;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :|| :|  |: |||:
Db      68 GNINPNSGGTNYNEKFK 84


RESULT   5
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ID   Q9UL92      PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;


  Query Match             53.8%;  Score 49;  DB 4;  Length 124;
  Best Local Similarity   47.1%;  Pred. No. 1.5;
  Matches    8;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           | :||: |  ::|:|||
Db      49 GIINPSGGSTSYAQKFQ 65


RESULT   6
Q96QS0
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:27 ; Search time 49.09 Seconds
(without alignments)
8.459 Million cell updates/sec

Title: US-09-780-035-10
Perfect score: 91
Sequence: 1 GRLNPTTGDANFAEKFQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	63	69.2	123	1	US-08-477-877B-94	Sequence 94, Appl
2	63	69.2	123	2	US-08-472-281A-94	Sequence 94, Appl
3	63	69.2	123	2	US-08-477-989B-94	Sequence 94, Appl
4	58	63.7	123	1	US-08-497-312-15	Sequence 15, Appl
5	58	63.7	123	1	US-08-497-312-17	Sequence 17, Appl
6	58	63.7	123	2	US-08-560-558E-28	Sequence 28, Appl
7	57	62.6	117	4	US-09-025-769B-22	Sequence 22, Appl
8	55	60.4	117	3	US-08-545-809A-90	Sequence 90, Appl
9	55	60.4	120	4	US-09-025-769B-36	Sequence 36, Appl
10	55	60.4	120	4	US-09-025-769B-59	Sequence 59, Appl
11	55	60.4	128	1	US-08-276-852-53	Sequence 53, Appl
12	55	60.4	128	1	US-08-276-852-55	Sequence 55, Appl
13	55	60.4	128	1	US-08-276-852-56	Sequence 56, Appl
14	55	60.4	128	1	US-08-899-575-53	Sequence 53, Appl
15	55	60.4	128	1	US-08-899-575-55	Sequence 55, Appl
16	55	60.4	128	1	US-08-899-575-56	Sequence 56, Appl
17	55	60.4	128	1	US-08-899-575-53	Sequence 53, Appl
18	55	60.4	128	1	US-08-899-575-55	Sequence 55, Appl
19	55	60.4	128	1	US-08-899-575-56	Sequence 56, Appl
20	55	60.4	128	5	PCT-US95-08743-53	Sequence 53, Appl
21	55	60.4	128	5	PCT-US95-08743-55	Sequence 55, Appl
22	55	60.4	128	5	PCT-US95-08743-56	Sequence 56, Appl
23	54	59.3	17	2	US-08-560-558E-33	Sequence 33, Appl
24	54	59.3	105	2	US-08-793-490-10	Sequence 10, Appl
25	54	59.3	117	4	US-09-157-370-2	Sequence 2, Appli
26	54	59.3	118	2	US-08-232-081B-8	Sequence 8, Appli
27	54	59.3	118	2	US-08-232-081B-38	Sequence 38, Appl
28	54	59.3	128	1	US-08-276-852-58	Sequence 58, Appl
29	54	59.3	128	1	US-08-899-575-58	Sequence 58, Appl
30	54	59.3	128	1	US-08-899-575-58	Sequence 58, Appl
31	54	59.3	128	5	PCT-US95-08743-58	Sequence 58, Appl
32	53	58.2	102	1	US-07-834-539A-55	Sequence 55, Appl
33	53	58.2	102	1	US-08-053-131-63	Sequence 63, Appl
34	53	58.2	102	1	US-08-645-641-63	Sequence 63, Appl
35	53	58.2	102	1	US-07-853-408B-63	Sequence 63, Appl
36	53	58.2	102	2	US-08-096-762-63	Sequence 63, Appl
37	53	58.2	102	2	US-08-800-353-55	Sequence 55, Appl
38	53	58.2	102	2	US-08-308-865-63	Sequence 63, Appl
39	53	58.2	102	5	PCT-US92-06185-55	Sequence 55, Appl
40	53	58.2	102	5	PCT-US92-10983-63	Sequence 63, Appl
41	53	58.2	116	2	US-08-737-560A-7	Sequence 7, Appli
42	53	58.2	117	4	US-09-042-353-232	Sequence 232, App
43	53	58.2	117	4	US-08-758-417A-80	Sequence 80, Appl
44	53	58.2	147	2	US-08-579-940-4	Sequence 4, Appli
45	53	58.2	147	4	US-08-838-692-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,877B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polypeptide
;    FEATURE:
;      NAME/KEY:  Human Amu 5-3 heavy chain variable region.
US-08-477-877B-94
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  Query Match             69.2%;  Score 63;  DB 1;  Length 123;
  Best Local Similarity   58.8%;  Pred. No. 0.0011;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
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Db      49 GRINPNSGGTNYAQKFQ 65


RESULT   2
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,281A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polypeptide
;    FEATURE:
;      NAME/KEY:  Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94


  Query Match             69.2%;  Score 63;  DB 2;  Length 123;
  Best Local Similarity   58.8%;  Pred. No. 0.0011;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      49 GRINPNSGGTNYAQKFQ 65


RESULT   3
US-08-477-989B-94
; Sequence 94, Application US/08477989B
; Patent No. 5951983
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    APPLICANT:  Kaplan, Ruth
;    APPLICANT:  Kieber-Emmons, Thomas
;    APPLICANT:  Postema, Christina E.
;    APPLICANT:  White-Scharf, Mary
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses
;    TITLE OF INVENTION:  Thereof for Inhibiting
;    TITLE OF INVENTION:  T-Cell Activation and
;    TITLE OF INVENTION:  Proliferation
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,989B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polypeptide
;    FEATURE:
;      NAME/KEY:  Human Amu 5-3 heavy chain variable
;      NAME/KEY:  region.
US-08-477-989B-94


  Query Match             69.2%;  Score 63;  DB 2;  Length 123;
  Best Local Similarity   58.8%;  Pred. No. 0.0011;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GRLNPTTGDANFAEKFQ 17
           ||:|| :|  |:|:|||
Db      49 GRINPNSGGTNYAQKFQ 65


RESULT   4
US-08-497-312-15
; Sequence 15, Application US/08497312
; Patent No. 5712120
;  GENERAL INFORMATION:
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:25:35 ; Search time 61.61 Seconds
(without alignments)
6.239 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	40	2	E64988	hypothetical prote
2	20	100.0	40	2	H71330	hypothetical prote
3	20	100.0	44	2	I48942	cellular disintegr
4	20	100.0	47	2	A59009	diuretic hormone 2
5	20	100.0	52	2	H81124	hypothetical prote
6	20	100.0	54	2	S45255	yjjX protein homol
7	20	100.0	54	2	T42357	hypothetical prote
8	20	100.0	57	2	JN0739	hypothetical 6.4K
9	20	100.0	60	2	JN0741	hypothetical 6.6K
10	20	100.0	61	2	T47055	hypothetical prote
11	20	100.0	63	2	C95851	hypothetical prote
12	20	100.0	65	2	A72368	hypothetical prote
13	20	100.0	67	2	S45258	yjjX protein homol
14	20	100.0	67	2	E95210	hypothetical prote
15	20	100.0	67	2	A81189	hypothetical prote
16	20	100.0	67	2	H98074	hypothetical prote
17	20	100.0	68	2	A25574	molybdenum-pterin-
18	20	100.0	68	2	A29094	molybdenum-pterin-
19	20	100.0	71	2	G90533	hypothetical prote
20	20	100.0	71	2	G83792	hypothetical prote
21	20	100.0	74	2	C81738	conserved hypothet
22	20	100.0	75	1	BVECRY	traY protein - Esc
23	20	100.0	76	2	A87655	ribosomal protein
24	20	100.0	77	2	T41510	hypothetical prote
25	20	100.0	82	2	S76249	ribosomal protein
26	20	100.0	83	2	B70870	hypothetical prote
27	20	100.0	83	2	T03673	pitl protein (clon
28	20	100.0	85	2	T21842	hypothetical prote
29	20	100.0	87	2	C99587	hypothetical prote
30	20	100.0	88	2	H90151	conserved hypothet
31	20	100.0	92	2	T12826	histone-like DNA-b
32	20	100.0	93	2	T17447	hypothetical prote
33	20	100.0	93	2	AC0232	probable transcrip
34	20	100.0	93	2	AC3330	hypothetical prote
35	20	100.0	94	2	JH0237	repressor protein
36	20	100.0	94	2	E95332	hypothetical prote
37	20	100.0	94	2	AD1459	B. subtilis transc
38	20	100.0	94	2	AI1095	B. subtilis transc
39	20	100.0	94	2	C98239	hypothetical prote
40	20	100.0	95	2	G86438	protein T19E23.5 [
41	20	100.0	96	2	S03096	transition state r
42	20	100.0	96	2	AG0229	conserved hypothet
43	20	100.0	99	1	QSBPB7	host specificity p
44	20	100.0	99	2	D82929	ATP synthase delta
45	20	100.0	104	2	AD3464	hypothetical prote

ALIGNMENTS

RESULT 1
E64988
hypothetical protein b2191 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: E64988
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; .A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: E64988
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-40 <BLAT>
A;Cross-references: GB:AE000308; GB:U00096; NID:g1788508; PIDN:AAC75251.1; PID:g17885
A;Experimental source: strain K-12, substrain MG1655

Query Match 100.0%; Score 20; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 5 KEGA 8

RESULT 2
H71330
hypothetical protein TP0382 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: H71330
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: H71330
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-40 <COL>
A;Cross-references: GB:AE001217; GB:AE000520; NID:g3322656; PIDN:AAC65383.1; PID:g332
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0382

Query Match 100.0%; Score 20; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db      6 KEGA 9
```

RESULT 3
I48942
cellular disintegrin-related protein 16-1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
C;Accession: I48942
R;Weskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A;Title: A new family of cellular proteins related to snake venom disintegrins.
A;Reference number: A53476; MUID:94195820
A;Accession: I48942
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-44 <RES>
A;Cross-references: EMBL:U06144; NID:g487136; PIDN:AAA18423.1; PID:g487137
C;Superfamily: unassigned disintegrins; disintegrin homology

Query Match 100.0%; Score 20; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db     16 KEGA 19
```

RESULT 4
A59009
diuretic hormone 2 - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 10-Oct-1997 #sequence_revision 10-Oct-1997 #text_change 26-Feb-1998
C;Accession: A59009
R;Furuya, K.; Schegg, K.M.; Schooley, D.A.
submitted to the Protein Sequence Database, August 1997
A;Description: Isolation and Identification of a Second Diuretic Hormone from Tenebrio m
A;Reference number: A59009
A;Accession: A59009
A;Molecule type: protein
A;Residues: 1-47 <SCH>
C;Superfamily: diuretic hormone precursor; diuretic hormone homology
F;47/Modified site: amidated carboxyl end (Leu) #status absent

Query Match 100.0%; Score 20; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db     34 KEGA 37
```

RESULT 5
H81124
hypothetical protein NMB1079 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: H81124
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Accession: H81124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <TET>
A;Cross-references: GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF41472.1; PID:g722
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1079

Query Match 100.0%; Score 20; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db     37 KEGA 40
```

RESULT 6
S45255
yjjX protein homolog - Enterobacter aerogenes (fragment)
C;Species: Enterobacter aerogenes
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 08-Oct-1999
C;Accession: S45255
R;Arvidson, D.N.; Arvidson, C.G.; Lawson, C.L.; Miner, J.; Adams, C.; Youderian, P.
Nucleic Acids Res. 22, 1821-1829, 1994
A;Title: The tryptophan repressor sequence is highly conserved among the Enterobacter
A;Reference number: S45254; MUID:94268903
A;Accession: S45255
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-54 <ARV>
A;Cross-references: EMBL:L26582; NID:g433053; PIDN:AAC36893.1; PID:g433055
A;Experimental source: ATCC 13048
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
C;Superfamily: Escherichia coli conserved yjjX protein

Query Match 100.0%; Score 20; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db     19 KEGA 22
```

RESULT 7
T42357
hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: T42357
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus sub
A;Reference number: Z22137; MUID:98094274
A;Accession: T42357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-54 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66511.1

Query Match 100.0%; Score 20; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 KEGA 4
          ||||
Db     50 KEGA 53
```

RESULT 8
JN0739
hypothetical 6.4K protein - phage SPP1
N;Alternate names: hypothetical protein 48
C;Species: phage SPP1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: JN0739; S21437
R;Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A;Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1 g
A;Reference number: JN0729; MUID:93328123
A;Accession: JN0739
A;Molecule type: DNA
A;Residues: 1-57 <CHA>
A;Cross-references: EMBL:X65941; NID:g14843; PIDN:CAA46752.1; PID:g579086

Query Match 100.0%; Score 20; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 53 KEGA 56

RESULT 9
JN0741
hypothetical 6.6K protein - phage SPP1
N;Alternate names: hypothetical protein 50
C;Species: phage SPP1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-May-2000
C;Accession: JN0741; T42359; S21439
R;Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A;Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1 g
A;Reference number: JN0729; MUID:93328123
A;Accession: JN0741
A;Molecule type: DNA
A;Residues: 1-60 <CHA>
A;Cross-references: EMBL:X65941; NID:g14843; PIDN:CAA46754.1; PID:g579088
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; MUID:98094274
A;Accession: T42359
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-60 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66513.1

Query Match 100.0%; Score 20; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 56 KEGA 59

RESULT 10
T47055
hypothetical protein [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: T47055
R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel
submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: Z24348
A;Accession: T47055
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-61 <BUC>
A;Cross-references: EMBL:AL031866; PIDN:CAA21398.1
A;Experimental source: strain 6/69

Query Match 100.0%; Score 20; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 28 KEGA 31

RESULT 11
C95851
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pS
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: C95851
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C95851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48475.1; PID:g15139947; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20075
A;Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 5 KEGA 8

RESULT 12
A72368
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72368
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
A;Accession: A72368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <ARN>
A;Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AAD35592.1; PID:g498
A;Experimental source: strain MSB8

C;Genetics:
A;Gene: TM0507

Query Match 100.0%; Score 20; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 52 KEGA 55

RESULT 13
S45258
yjjX protein homolog - Enterobacter cloacae (fragment)
C;Species: Enterobacter cloacae
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 08-Oct-1999
C;Accession: S45258
R;Arvidson, D.N.; Arvidson, C.G.; Lawson, C.L.; Miner, J.; Adams, C.; Youderian, P.
Nucleic Acids Res. 22, 1821-1829, 1994
A;Title: The tryptophan repressor sequence is highly conserved among the Enterobacteriac
A;Reference number: S45254; MUID:94268903
A;Accession: S45258
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-67 <ARV>
A;Cross-references: EMBL:L26583; NID:g433056; PIDN:AAA20184.1; PID:g433059
A;Experimental source: ATCC 23355
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
C;Superfamily: Escherichia coli conserved yjjX protein

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 32 KEGA 35

RESULT 14
E95210
hypothetical protein SP1805 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: E95210
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75878.1; PID:g14973304; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1805

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 29 KEGA 32

RESULT 15
A81189
hypothetical protein NMB0519 [imported] - Neisseria meningitidis (strain MC58 serogro
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: A81189
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Accession: A81189
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <TET>
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40951.1; PID:g722
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0519

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 63 KEGA 66

Search completed: June 12, 2002, 11:25:37
Job time: 302 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:39:13 ; Search time 29.47 Seconds
(without alignments)
5.255 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

T[redacted] number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	40	1	Y382_TREPA	O83397 treponema p
2	20	100.0	47	1	DIU2_TENMO	P56619 tenebrio mo
3	20	100.0	54	1	YJJX_ENTAE	P39430 enterobacte
4	20	100.0	55	1	PHNS_DESVH	Q06173 desulfovibr
5	20	100.0	67	1	YJJX_ENTCL	P39431 enterobacte
6	20	100.0	68	1	MOP1_CLOPA	P04952 clostridium
7	20	100.0	68	1	MOP2_CLOPA	P08854 clostridium
8	20	100.0	75	1	TRY3_ECOLI	P05835 escherichia
9	20	100.0	76	1	RL31_CAUCR	Q9a3c9 caulobacter
10	20	100.0	82	1	RS16_SYNY3	P74410 synechocyst
11	20	100.0	92	1	DBH2_BACSU	O31946 bacillus su
12	20	100.0	94	1	SCRR_VIBAL	P24508 vibrio algi
13	20	100.0	96	1	ABRB_BACSU	P08874 bacillus su
14	20	100.0	99	1	VHSB_BPT7	P03751 bacteriopha
15	20	100.0	106	1	RL3E_SULTO	P58376 sulfolobus
16	20	100.0	110	1	GRX1_YEAST	P25373 saccharomyc
17	20	100.0	114	1	SYC1_RAT	P51672 rattus norv
18	20	100.0	116	1	Y789_METJA	Q58199 methanococc
19	20	100.0	120	1	YE55_PYRHO	O59124 pyrococcus
20	20	100.0	122	1	RL7_PSEAE	Q9hwc8 pseudomonas
21	20	100.0	122	1	RTP_BACSU	P14382 bacillus su
22	20	100.0	124	1	RL7_BRUME	P41106 brucella me
23	20	100.0	126	1	DHA5_BOVIN	P52476 bos taurus
24	20	100.0	126	1	RK12_CYAPA	P48124 cyanophorá
25	20	100.0	127	1	RBFA_BORBU	O51742 borrelia bu
26	20	100.0	129	1	AZU2_METJ	P12335 methylomona
27	20	100.0	129	1	RK12_PORPU	P51339 porphyra pu
28	20	100.0	139	1	Y024_METJA	Q60334 methanococc
29	20	100.0	140	1	HSLJ_ECOLI	P52644 escherichia
30	20	100.0	140	1	RS12_CAEEL	P49196 caenorhabdi
31	20	100.0	146	1	Y328_METJA	Q57774 methanococc
32	20	100.0	149	1	FUR_BACSU	P54574 bacillus su
33	20	100.0	150	1	TTHY_PIG	P50390 sus scrofa
34	20	100.0	153	1	YL54_ARCFU	O28128 archaeoglob
35	20	100.0	154	1	F6A2_ECOLI	P53509 escherichia
36	20	100.0	155	1	HS21_PHANI	Q01544 pharbitis n
37	20	100.0	156	1	RISB_HELPJ	Q9zn56 helicobacte
38	20	100.0	156	1	RS10_LUMRU	O77302 lumbricus r
39	20	100.0	159	1	HS21_SOYBN	P05477 glycine max
40	20	100.0	160	1	KAFK_PHYPO	P80197 physarum po
41	20	100.0	160	1	YG01_METJA	Q58996 methanococc
42	20	100.0	165	1	RL10_STRPY	P82480 streptococc
43	20	100.0	165	1	VEAE_BPP22	Q03547 bacteriopha
44	20	100.0	165	1	Y051_HAEIN	P44484 haemophilus
45	20	100.0	168	1	TCTP_BRAOL	Q944w6 brassica ol

ALIGNMENTS

RESULT 1
Y382_TREPA
ID Y382_TREPA STANDARD; PRT; 40 AA.
AC O83397;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0382.
GN TP0382.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
RL Science 281:375-388(1998).
CC ---
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CC ---
DR EMBL; AE001217; AAC65383.1; -.
DR TIGR; TP0382; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 40 AA; 4104 MW; 1B74B6D9597CCC90 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 6 KEGA 9

RESULT 2
DIU2_TENMO
ID DIU2_TENMO STANDARD; PRT; 47 AA.
AC P56619;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

```
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Diuretic hormone II (DH II) (Diuretic peptide II) (DP II) (DH(47)).
OS   Tenebrio molitor (Yellow mealworm).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Cucujiformia; Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RX   MEDLINE=98283334; PubMed=9622015;
RA   Furuya K., Schegg K.M., Schooley D.A.;
RT   "Isolation and identification of a second diuretic hormone from
RT   Tenebrio molitor.";
RL   Peptides 19:619-626(1998).
CC   -!- FUNCTION: INCREASES CYCLIC AMP PRODUCTION IN MALPIGHIAN TUBULES.
CC   -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC       FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
DR   InterPro; IPR000187; CRF.
DR   InterPro; IPR003621; Diurtc_hormn.
DR   Pfam; PF00473; CRF; 1.
DR   ProDom; PD014750; Diurtc_hormn; 1.
DR   SMART; SM00039; CRF; 1.
DR   PROSITE; PS00511; CRF; 1.
KW   Hormone.
SQ   SEQUENCE   47 AA;  5030 MW;  9176E090AB1B803A CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db      34 KEGA 37


RESULT   3
YJJX_ENTAE
ID   YJJX_ENTAE     STANDARD;      PRT;    54 AA.
AC   P39430;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Hypothetical protein in trpR 3'region (Fragment).
GN   YJJX.
OS   Enterobacter aerogenes (Aerobacter aerogenes).
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Enterobacter.
OX   NCBI_TaxID=548;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94268903; PubMed=8208606;
RA   Arvidson D.N., Arvidson C.G., Lawson C.L., Miner J., Adams C.,
RA   Youderian P.;
RT   "The tryptophan repressor sequence is highly conserved among the
RT   Enterobacteriaceae.";
RL   Nucleic Acids Res. 22:1821-1829(1994).
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; L26582; AAC36893.1; -.
DR   InterPro; IPR002786; DUF84.
DR   ProDom; PD016591; DUF84; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   54 AA;  5794 MW;  23A9E94ED9FA0FC5 CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db      19 KEGA 22


RESULT   4
PHNS_DESVH
ID   PHNS_DESVH     STANDARD;      PRT;    55 AA.
AC   Q06173;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Periplasmic [NiFe] hydrogenase small subunit precursor (EC 1.18.99.1)
DE   (NiFe hydrogenlyase small chain) (Fragment).
OS   Desulfovibrio vulgaris (strain Hildenborough).
OC   Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
OX   NCBI_TaxID=882;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-28.
RX   MEDLINE=93123973; PubMed=1479348;
RA   Niviere V., Wong S.L., Voordouw G.;
RT   "Site-directed mutagenesis of the hydrogenase signal peptide
RT   consensus box prevents export of a beta-lactamase fusion protein.";
RL   J. Gen. Microbiol. 138:2173-2183(1992).
CC   -!- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized
CC       ferredoxin + H(2).
CC   -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS AND ONE 3FE-4S CLUSTER.
CC   -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
CC   -!- SUBCELLULAR LOCATION: Periplasmic.
CC   -!- MISCELLANEOUS: [FE], [NIFE], AND [NIFESE] HYDROGENASES APPEAR TO
CC       REPRESENT THREE DISTINCT ENZYMES HAVING HYDROGENASE ACTIVITY.
KW   Oxidoreductase; Periplasmic; Iron-sulfur; 4Fe-4S; 3Fe-4S; Signal.
FT   SIGNAL        1     49       POTENTIAL.
FT   CHAIN        50    >55       PERIPLASMIC [NIFE] HYDROGENASE SMALL
FT                                SUBUNIT.
FT   MUTAGEN      18     18       R->E: COMPLETELY INHIBITED EXPORT AND
FT                                PROCESSING OF THE FUSION PROTEIN.
FT   NON_TER      55     55
SQ   SEQUENCE   55 AA;  5930 MW;  E865200656D8A9DC CRC64;

  Query Match             100.0%;  Score 20;  DB 1;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 77;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db       9 KEGA 12


RESULT   5
YJJX_ENTCL
ID   YJJX_ENTCL     STANDARD;      PRT;    67 AA.
AC   P39431;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein in trpR 3'region (Fragment).
GN   YJJX.
OS   Enterobacter cloacae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Enterobacter.
OX   NCBI_TaxID=550;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94268903; PubMed=8208606;
RA   Arvidson D.N., Arvidson C.G., Lawson C.L., Miner J., Adams C.,
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:38:38 ; Search time 107.96 Seconds
(without alignments)
6.410 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

T[redacted] number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

[redacted] Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	27	4	Q9BS88	Q9bs88 homo sapien
2	20	100.0	34	13	Q9PTK8	Q9ptk8 brachydanio
3	20	100.0	37	11	O55073	O55073 mus musculu
4	20	100.0	40	16	P76451	P76451 escherichia
5	20	100.0	52	16	Q9JZF4	Q9jzf4 neisseria m
6	20	100.0	54	9	O48497	O48497 bacteriopha
7	20	100.0	57	9	Q38078	Q38078 bacteriopha
8	20	100.0	60	9	Q38080	Q38080 bacteriopha
9	20	100.0	61	2	Q9X9G5	Q9x9g5 yersinia ps
10	20	100.0	63	16	Q92X87	Q92x87 rhizobium m
11	20	100.0	64	7	Q30816	Q30816 ovis aries
12	20	100.0	64	7	Q30820	Q30820 ovis aries
13	20	100.0	65	16	Q9WYX7	Q9wyx7 thermotoga
14	20	100.0	66	16	Q99XV5	Q99xv5 streptococc
15	20	100.0	67	16	Q9K0R1	Q9k0r1 neisseria m
16	20	100.0	67	16	Q97P39	Q97p39 streptococc
17	20	100.0	68	4	Q16278	Q16278 homo sapien
18	20	100.0	71	16	Q9KDR8	Q9kdr8 bacillus ha
19	20	100.0	71	16	Q98R35	Q98r35 mycoplasma
20	20	100.0	74	16	Q9PLH0	Q9plh0 chlamydia m
21	20	100.0	83	10	Q40539	Q40539 nicotiana t
22	20	100.0	83	16	O53222	O53222 mycobacteri
23	20	100.0	85	5	Q9XV39	Q9xv39 caenorhabdi
24	20	100.0	87	5	Q9GS26	Q9gs26 ancylostoma
25	20	100.0	87	16	Q98PW6	Q98pw6 mycoplasma
26	20	100.0	88	2	Q9L2L7	Q91217 streptomyce
27	20	100.0	88	17	Q980Z7	Q980z7 sulfolobus
28	20	100.0	89	2	Q9EWN5	Q9ewn5 streptomyce
29	20	100.0	90	2	Q9S524	Q9s524 escherichia
30	20	100.0	93	2	Q9ZFZ8	Q9zfz8 yersinia pe
31	20	100.0	94	13	Q90ZF0	Q90zf0 gallus gall
32	20	100.0	94	16	Q92ZC5	Q92zc5 rhizobium m
33	20	100.0	94	16	Q92F95	Q92f95 listeria in
34	20	100.0	95	6	Q9GJZ9	Q9gjz9 callithrix
35	20	100.0	95	10	Q9SHF5	Q9shf5 arabidopsis
36	20	100.0	96	2	O34282	O34282 yersinia pe
37	20	100.0	97	10	Q42255	Q42255 arabidopsis
38	20	100.0	98	2	Q52096	Q52096 pseudomonas
39	20	100.0	99	16	Q9PR11	Q9pr11 ureaplasma
40	20	100.0	102	17	Q973V1	Q973v1 sulfolobus
41	20	100.0	104	2	P94757	P94757 escherichia
42	20	100.0	106	2	Q44480	Q44480 anabaena va
43	20	100.0	106	3	Q07989	Q07989 saccharomyc
44	20	100.0	106	4	Q9H4N4	Q9h4n4 homo sapien
45	20	100.0	106	7	Q31261	Q31261 rattus norv

ALIGNMENTS

RESULT 1
Q9BS88
ID Q9BS88 PRELIMINARY; PRT; 27 AA.
AC Q9BS88;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO CHAPERONIN CONTAINING TCP1, SUBUNIT 8 (THETA).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, PRIMITIVE NEUROECTODERMAL;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC005220; AAH05220.1; -.
SQ SEQUENCE 27 AA; 2894 MW; 430CB0FB04967B0E CRC64;

Query Match 100.0%; Score 20; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 KEGA 4
           ||||
Db      16 KEGA 19
```

RESULT 2
Q9PTK8
ID Q9PTK8 PRELIMINARY; PRT; 34 AA.
AC Q9PTK8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REGGIE2 (FRAGMENT).
GN FLOT1 OR REGGIE2.

```
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20261668; PubMed=10799891;
RA   Michalova V., Murray B.W., Sultmann H., Klein J.;
RT   "A contig map of the Mhc class I genomic region in the zebrafish
RT   reveals ancient synteny.";
RL   J. Immunol. 164:5296-5305(2000).
DR   EMBL; AF182161; AAF20177.1; -.
DR   ZFIN; ZDB-GENE-000210-36; flot1.
FT   NON_TER       1      1
FT   NON_TER      34     34
SQ   SEQUENCE   34 AA;  3881 MW;  BBDACFC53EF4E3F9 CRC64;


  Query Match           100.0%;  Score 20;  DB 13;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db      20 KEGA 23


RESULT   3
O55073
ID   O55073      PRELIMINARY;      PRT;    37 AA.
AC   O55073;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DECORIN (FRAGMENT).
GN   MDCN.
OS   Mus musculus domesticus (western European house mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10092;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kraus P., Just W., Vogel W.;
RT   "mDcn Intron 2 (XbaI) to Intron 3 (HincII).";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF047708; AAC04271.1; -.
DR   InterPro; IPR001611; LRR.
DR   Pfam; PF00560; LRR; 1.
FT   NON_TER       1      1
FT   NON_TER      37     37
SQ   SEQUENCE   37 AA;  4308 MW;  C04BBAAE0C843BC2 CRC64;


  Query Match           100.0%;  Score 20;  DB 11;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db      26 KEGA 29


RESULT   4
P76451
ID   P76451      PRELIMINARY;      PRT;    40 AA.
AC   P76451;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FROM BASES 2276392 TO 2288352 (SECTION 198 OF 400) OF THE COMPLETE
DE   GENOME.
GN   B2191.
```

```
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
DR   EMBL; AE000308; AAC75251.1; -.
KW   Complete proteome.
SQ   SEQUENCE   40 AA;  4591 MW;  56C974E4D666B54D CRC64;


  Query Match           100.0%;  Score 20;  DB 16;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 3.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db       5 KEGA 8


RESULT   5
Q9JZF4
ID   Q9JZF4      PRELIMINARY;      PRT;    52 AA.
AC   Q9JZF4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN NMB1079.
GN   NMB1079.
OS   Neisseria meningitidis (serogroup B).
OC   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX   NCBI_TaxID=491;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MC58 / SEROGROUP B;
RX   MEDLINE=20175755; PubMed=10710307;
RA   Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA   Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA   Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA   Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA   Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA   Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA   Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA   Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT   "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT   MC58.";
RL   Science 287:1809-1815(2000).
DR   EMBL; AE002458; AAF41472.1; -.
DR   TIGR; NMB1079; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   52 AA;  6013 MW;  383F49EEB5A94FAE CRC64;


  Query Match           100.0%;  Score 20;  DB 16;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 4.3e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
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Db      37 KEGA 40


RESULT   6
O48497
ID   O48497      PRELIMINARY;      PRT;    54 AA.
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:32 ; Search time 136.11 Seconds
(without alignments)
3.264 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	4	22	AAG65301	Anti-IL-18 antibod
2	20	100.0	9	22	AAG99520	PRAME derived HLA-
3	20	100.0	10	22	AAG99418	PRAME derived HLA-
4	20	100.0	10	22	AAG83449	Arabidopsis thalia
5	20	100.0	12	18	AAW25324	Peptide clone LacI
6	20	100.0	18	22	ABB39285	Peptide #6791 enco
7	20	100.0	18	22	AAM59953	Human brain expres
8	20	100.0	18	22	AAM72552	Human bone marrow
9	20	100.0	18	22	AAM32792	Peptide #6829 enco
10	20	100.0	20	22	AAB55823	PL peptide #34. S
11	20	100.0	20	22	AAB57685	CC CKR-2 PL peptid
12	20	100.0	20	22	AAB58095	CC CKR-2 PL peptid
13	20	100.0	23	22	AAU00937	VH ligand-binding
14	20	100.0	25	20	AAY12805	Human 5' EST secre
15	20	100.0	27	22	AAG99548	HLA-A*0201 binding
16	20	100.0	27	22	AAG99550	HLA-A*0201 binding
17	20	100.0	29	22	ABB50871	Human secreted pro
18	20	100.0	30	22	ABB37950	Peptide #5456 enco
19	20	100.0	30	22	ABB23198	Protein #5197 enco
20	20	100.0	30	22	AAM58582	Human brain expres
21	20	100.0	30	22	AAM71083	Human bone marrow
22	20	100.0	30	22	AAM31360	Peptide #5397 enco
23	20	100.0	33	22	AAM73472	Human bone marrow
24	20	100.0	33	22	AAM33670	Peptide #7707 enco
25	20	100.0	34	22	ABG21965	Novel human diagno
26	20	100.0	36	21	AAY77861	T. ferrooxidans ty
27	20	100.0	37	20	AAY01202	Polypeptide fragme
28	20	100.0	38	20	AAY42833	Non-EPOR-binding c
29	20	100.0	39	16	AAR87205	Plasmodium knowlse
30	20	100.0	39	20	AAY02730	Human secreted pro
31	20	100.0	41	22	ABG28104	Novel human diagno
32	20	100.0	45	22	ABG10958	Novel human diagno
33	20	100.0	46	22	ABB36694	Peptide #4200 enco
34	20	100.0	46	22	ABB38283	Peptide #5789 enco
35	20	100.0	46	22	ABB23464	Protein #5463 enco
36	20	100.0	46	22	AAM58906	Human brain expres
37	20	100.0	46	22	AAM71428	Human bone marrow
38	20	100.0	46	22	AAM19077	Peptide #5511 enco
39	20	100.0	46	22	AAM31716	Peptide #5753 enco
40	20	100.0	47	20	AAY30879	Human secreted pro
41	20	100.0	49	22	ABB40684	Peptide #8190 enco
42	20	100.0	49	22	ABB24925	Protein #6924 enco
43	20	100.0	49	22	AAM61546	Human brain expres
44	20	100.0	49	22	AAM74334	Human bone marrow
45	20	100.0	49	22	AAM34447	Peptide #8484 enco

ALIGNMENTS

RESULT 1
AAG65301
ID AAG65301 standard; protein; 4 AA.
XX
AC AAG65301;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain CDR3 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 25; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain CDR3 fragment.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 1 kega 4

RESULT 2
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ID AAG99520 standard; Peptide; 9 AA.
XX
AC AAG99520;
XX
DT 01-OCT-2001 (first entry)
XX
DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 162.
XX
KW Vaccine; immune response; T cell response; epitope; proteasome;
KW cancer; infection.
XX
OS Unidentified.
XX
PN EP1118860-A1.
XX
PD 25-JUL-2001.
XX
PF 21-JAN-2000; 2000EP-0200242.
XX
PR 21-JAN-2000; 2000EP-0200242.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX
PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;
XX
DR WPI; 2001-427158/46.
XX
PT Selecting and/or producing a T cell epitope useful in a vaccine
PT comprises subjecting a precursor peptide or polypeptide to the action
PT of a 20S proteasome to determine the location of the C-terminus -
XX
PS Disclosure; Page 77; 102pp; English.
XX
CC The present invention describes a method of producing T cell epitopes,
CC involving subjecting a precursor peptide to the action of a 20S
CC proteasome, in order to locate the C-terminus of said epitope. This can
CC be used in the production of vaccines, which can then be used to provoke
CC a T cell response in the treatment of diseases such as cancer and
CC infections. The present sequence is a peptide described in the
CC exemplification of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 5 kega 8

RESULT 3
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ID AAG99418 standard; Peptide; 10 AA.
XX
AC AAG99418;
XX
DT 01-OCT-2001 (first entry)
XX
DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 60.
XX
KW Vaccine; immune response; T cell response; epitope; proteasome;
KW cancer; infection.
XX
OS Unidentified.
XX
PN EP1118860-A1.
XX
PD 25-JUL-2001.
XX
PF 21-JAN-2000; 2000EP-0200242.
XX
PR 21-JAN-2000; 2000EP-0200242.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX
PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;
XX
DR WPI; 2001-427158/46.
XX
PT Selecting and/or producing a T cell epitope useful in a vaccine
PT comprises subjecting a precursor peptide or polypeptide to the action
PT of a 20S proteasome to determine the location of the C-terminus -
XX
PS Disclosure; Page 40; 102pp; English.
XX
CC The present invention describes a method of producing T cell epitopes,
CC involving subjecting a precursor peptide to the action of a 20S
CC proteasome, in order to locate the C-terminus of said epitope. This can
CC be used in the production of vaccines, which can then be used to provoke
CC a T cell response in the treatment of diseases such as cancer and
CC infections. The present sequence is a peptide described in the
CC exemplification of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 3 kega 6

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:27 ; Search time 49.09 Seconds
(without alignments)
1.990 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

[redacted] number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	12	1	US-08-548-540-162	Sequence 162, App
2	20	100.0	12	5	PCT-US96-09809-162	Sequence 162, App
3	20	100.0	20	2	US-07-952-853-17	Sequence 17, Appl
4	20	100.0	20	2	US-08-914-848-17	Sequence 17, Appl
5	20	100.0	30	3	US-08-467-023-261	Sequence 261, App
6	20	100.0	39	4	US-09-227-357-230	Sequence 230, App
7	20	100.0	47	4	US-09-261-855-17	Sequence 17, Appl
8	20	100.0	55	1	US-07-869-912-4	Sequence 4, Appli
9	20	100.0	112	4	US-08-936-165A-338	Sequence 338, App
10	20	100.0	144	4	US-08-858-207A-523	Sequence 523, App
11	20	100.0	151	2	US-08-913-477-11	Sequence 11, Appl
12	20	100.0	169	1	US-08-441-629-2	Sequence 2, Appli
13	20	100.0	169	3	US-08-776-207-2	Sequence 2, Appli
14	20	100.0	169	5	PCT-US95-09172-2	Sequence 2, Appli
15	20	100.0	170	2	US-08-913-477-21	Sequence 21, Appl
16	20	100.0	234	3	US-08-836-236-7	Sequence 7, Appli
17	20	100.0	235	4	US-08-944-483-65	Sequence 65, Appl
18	20	100.0	239	4	US-09-485-885-12	Sequence 12, Appl
19	20	100.0	241	4	US-09-382-155-21	Sequence 21, Appl
20	20	100.0	241	4	US-09-074-044A-21	Sequence 21, Appl
21	20	100.0	249	2	US-08-991-946A-1	Sequence 1, Appli
22	20	100.0	270	5	PCT-US93-03035-2	Sequence 2, Appli
23	20	100.0	273	4	US-08-928-213B-13	Sequence 13, Appl
24	20	100.0	287	1	US-08-365-981-12	Sequence 12, Appl
25	20	100.0	292	4	US-09-485-885-10	Sequence 10, Appl
26	20	100.0	294	2	US-08-701-191A-17	Sequence 17, Appl
27	20	100.0	299	4	US-09-621-233-2	Sequence 2, Appli
28	20	100.0	317	4	US-09-390-326-5	Sequence 5, Appli
29	20	100.0	320	2	US-08-933-750C-12	Sequence 12, Appl
30	20	100.0	320	4	US-09-234-613-12	Sequence 12, Appl
31	20	100.0	323	4	US-09-462-844-4	Sequence 4, Appli
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33	20	100.0	325	4	US-09-042-785A-9	Sequence 9, Appli
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35	20	100.0	344	1	US-07-941-523-24	Sequence 24, Appl
36	20	100.0	344	4	US-09-318-448-21	Sequence 21, Appl
37	20	100.0	351	1	US-09-500-651-2	Sequence 2, Appli
38	20	100.0	351	2	US-08-813-591-2	Sequence 2, Appli
39	20	100.0	367	4	US-09-390-326-9	Sequence 9, Appli
40	20	100.0	367	4	US-09-390-326-12	Sequence 12, Appl
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42	20	100.0	374	4	US-08-446-669-2	Sequence 2, Appli
43	20	100.0	374	4	US-09-091-405-2	Sequence 2, Appli
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45	20	100.0	377	4	US-09-352-990-28	Sequence 28, Appl

ALIGNMENTS

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RESULT 1
US-08-548-540-162
; Sequence 162, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
;   APPLICANT: Schatz, Peter J.
;   APPLICANT: Cull, Millard G.
;   APPLICANT: Miller, Jeff F.
;   APPLICANT: Stemmer, Willem P.C.
;   APPLICANT: Gates, Christian M.
;   TITLE OF INVENTION: Peptide Library and Screening Method
;   NUMBER OF SEQUENCES: 162
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: William M. Smith
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/548,540
;     FILING DATE: 26-OCT-1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/290,641
;     FILING DATE: 15-AUG-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/963,321
;     FILING DATE: 15-OCT-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William M.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 16528J-001240US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 162:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 12 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-548-540-162
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  Best Local Similarity  100.0%;  Pred. No. 32;
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Qy       1 KEGA 4
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Db       5 KEGA 8


RESULT   2
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; Sequence 162, Application PC/TUS9609809
;  GENERAL INFORMATION:
;     APPLICANT:  Schatz, Peter J.
;     APPLICANT:  Cull, Millard G.
;     APPLICANT:  Miller, Jeff F.
;     APPLICANT:  Stemmer, Willem P.C.
;     APPLICANT:  Gates, Christian M.
;     TITLE OF INVENTION:  Peptide Library and Screening Method
;     NUMBER OF SEQUENCES:  162
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  William M. Smith
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/09809
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/548,540
;       FILING DATE:  26-OCT-1995
;       APPLICATION NUMBER:  US 08/290,641
;       FILING DATE:  15-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/963,321
;       FILING DATE:  15-OCT-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  16528J-001240US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  162:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US96-09809-162


  Query Match           100.0%;  Score 20;  DB 5;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 32;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
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Db       5 KEGA 8


RESULT   3
US-07-952-853-17
; Sequence 17, Application US/07952853
; Patent No. 5863783
;  GENERAL INFORMATION:
;     APPLICANT:  Van Heuvel, Margaretha
;     APPLICANT:  Bakhuis, Janna G.
;     APPLICANT:  Coutel, Yves
;     APPLICANT:  Harder, Abraham
;     APPLICANT:  De Graaff, Leendert H.
;     APPLICANT:  Flipphi, Michel J. A.
;     APPLICANT:  Van Der Veen, Peter
;     APPLICANT:  Visser, Jacob
;     APPLICANT:  Andreoli, Peter M.
;     TITLE OF INVENTION:  CLONING AND EXPRESSION OF DNA
;     TITLE OF INVENTION:  MOLECULES
;     TITLE OF INVENTION:  ENCODING ARABINAN-DEGRADING ENZYMES OF FUNGAL
;     TITLE OF INVENTION:  ORIGIN
;     NUMBER OF SEQUENCES:  24
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORRISON & FOERSTER
;       STREET:  755 Page Mill Road
;       CITY:  Palo Alto
;       STATE:  California
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/952,853
;       FILING DATE:  19921125
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  246152003500
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-813-5600
;       TELEFAX:  415-494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  Aspergillus niger
US-07-952-853-17


  Query Match           100.0%;  Score 20;  DB 2;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 53;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEGA 4
           ||||
Db       2 KEGA 5


RESULT   4
US-08-914-848-17
; Sequence 17, Application US/08914848
; Patent No. 5989887
;  GENERAL INFORMATION:
;     APPLICANT:  Van Heuvel, Margaretha
;     APPLICANT:  Bakhuis, Janna G.
;     APPLICANT:  Coutel, Yves
;     APPLICANT:  Harder, Abraham
;     APPLICANT:  De Graaff, Leendert H.
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:33 ; Search time 136.11 Seconds
(without alignments)
8.977 Million cell updates/sec

Title: US-09-780-035-12
Perfect score: 64
Sequence: 1 QGDSLRHFYPN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	11	22	AAG65302	Anti-IL-18 antibod
2	64	100.0	109	22	AAG65309	Anti-IL-18 antibod
3	64	100.0	109	22	AAG65353	Anti-IL-18 antibod
4	56	87.5	11	22	AAG65305	Anti-IL-18 antibod
5	46	71.9	107	18	AAW15528	Anti-TGF beta-2 sc
6	44	68.8	108	22	AAG62935	Amino acid sequenc
7	44	68.8	108	22	AAG62945	Amino acid sequenc
8	44	68.8	108	22	AAG62961	Amino acid sequenc
9	44	68.8	109	18	AAW15559	TGF beta-1/TGF bet
10	44	68.8	109	22	AAU02504	Anti-adipocyte mon
11	43	67.2	109	16	AAR69091	Anti-HIV Fab tat10
12	43	67.2	109	18	AAW08740	Human anti-HIV Fab
13	43	67.2	318	18	AAW21746	E3330-binding prot
14	43	67.2	318	19	AAW48894	Homo sapiens AP en
15	43	67.2	318	19	AAW52864	Apurinic/apyrimidi
16	43	67.2	345	21	AAB56610	Human prostate can
17	43	67.2	524	19	AAW48893	Homo sapiens MGMT-
18	42	65.6	51	21	AAB09387	Hepatitis GB virus
19	42	65.6	3010	16	AAR95022	Hepatitis GB virus
20	40	62.5	250	19	AAW98373	H. pylori GHPO 110
21	40	62.5	418	20	AAW97650	Soybean SUG1 polyp
22	39	60.9	11	21	AAY95195	Anti-platelet glyc
23	39	60.9	11	21	AAY95216	Anti-platelet glyc
24	39	60.9	91	22	ABG13492	Novel human diagno
25	39	60.9	101	13	AAR22572	Light chain VL3.5
26	39	60.9	103	16	AAR80091	Human derived ligh
27	39	60.9	103	20	AAW95489	Human-derived RT3
28	39	60.9	104	22	AAG93606	Human anti-Rh(D) c
29	39	60.9	106	22	AAG93607	Human anti-Rh(D) c
30	39	60.9	106	22	AAU02531	Anti-adipocyte mon
31	39	60.9	107	16	AAR69092	Anti-HIV Fab tat10
32	39	60.9	107	18	AAW08741	Human anti-HIV Fab
33	39	60.9	107	21	AAY95194	Anti-platelet glyc
34	39	60.9	107	21	AAY95215	Anti-platelet glyc
35	39	60.9	107	22	AAG62969	Amino acid sequenc
36	39	60.9	108	21	AAY95179	Anti-platelet glyc
37	39	60.9	108	21	AAY95185	Anti-platelet glyc
38	39	60.9	108	21	AAY44616	Human antibody clo
39	39	60.9	108	22	AAG62933	Amino acid sequenc
40	39	60.9	108	22	AAG62937	Amino acid sequenc
41	39	60.9	108	22	AAG62939	Amino acid sequenc
42	39	60.9	108	22	AAU02632	Anti-adipocyte mon
43	39	60.9	109	18	AAW19884	CEA-specific antib
44	39	60.9	109	18	AAW15525	Anti-TGF beta-2 sc
45	39	60.9	109	18	AAW08583	Human antibody C4.

ALIGNMENTS

RESULT 1
AAG65302
ID AAG65302 standard; protein; 11 AA.
XX
AC AAG65302;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR1 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 27; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain CDR1 fragment.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 64; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||||||||
Db 1 qgdslrhfypn 11

RESULT 2
AAG65309
ID AAG65309 standard; protein; 109 AA.
XX
AC AAG65309;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47512.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 64; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||||||||
Db 23 qgdslrhfypn 33

RESULT 3
AAG65353
ID AAG65353 standard; protein; 109 AA.
XX
AC AAG65353;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47512.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 88; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 64; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||||||| |
Db 23 qgdslrhfypn 33

RESULT 4
AAG65305
ID AAG65305 standard; protein; 11 AA.
XX
AC AAG65305;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody variable region fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 29; Page 75; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody variable
CC region fragment.
XX
SQ Sequence 11 AA;

Query Match 87.5%; Score 56; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||||| |
Db 1 qgdslrhfysn 11

RESULT 5
AAW15528
ID AAW15528 standard; Protein; 107 AA.
XX
AC AAW15528;
XX
DT 27-NOV-1997 (first entry)
XX
DE Anti-TGF beta-2 scFv antibody 14F12 VL domain.
XX
KW Transforming growth factor beta-2; TGF-beta-2; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post-myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular didease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy; chain shuffling.
XX
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
PN GB2305921-A.
XX
PD 23-APR-1997.
XX
PF 07-OCT-1996; 96GB-0020920.
XX
PR 19-JAN-1996; 96GB-0001081.
PR 06-OCT-1995; 95GB-0020486.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
XX
DR WPI; 1997-215360/20.
DR N-PSDB; AAT60375.
XX
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
XX
PS Claim 5; Fig 2b(v); 184pp; English.
XX
CC This polypeptide sequence comprises the VL domain of human scFv
CC antibody 14F12, which is specific for transforming growth factor
CC (TGF) beta-2. It is encoded by a gene (AAT60375) isolated from a
CC light chain shuffle repertoire of a peripheral blood lymphocyte

CC library. The antigen-binding domains of human antibodies (see
CC AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the
CC adverse effects of TGF beta, such as (i) promotion of fibrosis (in
CC dermal, ocular or keloid scarring, lung fibrosis, arterial injury,
CC proliferative retinopathy, retinal detachment, adult respiratory
CC distress syndrome, liver cirrhosis, post myocardial infarction,
CC post-angioplasty restenosis, scleroderma, vascular disorders,
CC cataract, glaucoma, or esp. neural scarring and glomerulonephritis,
CC also (not claimed) osteoporosis), or (ii) immune and inflammatory
CC diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases
CC or macrophage pathogen infection). Nucleic acids encoding human
CC antibody VH and VL can be used for prodn. of recombinant antigen-
CC binding domains. These are highly specific, have low dissociation
CC constants (pref. less than 5 nM) and low IC50s for neutralisation.
XX
SQ Sequence 107 AA;

Query Match 71.9%; Score 46; DB 18; Length 107;
Best Local Similarity 72.7%; Pred. No. 0.5;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||::| |
Db 23 qgdslrnyyan 33

RESULT 6
AAG62935
ID AAG62935 standard; Protein; 108 AA.
XX
AC AAG62935;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone G67.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
27-NOV-2000; 2000WO-GB04501.
13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42379.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 92; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 108 AA;

Query Match 68.8%; Score 44; DB 22; Length 108;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
||||||:| |
Db 22 qgdslrsyytn 32

RESULT 7
AAG62945
ID AAG62945 standard; Protein; 108 AA.
XX
AC AAG62945;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone G79.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42389.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 97; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and

CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 108 AA;

Query Match 68.8%; Score 44; DB 22; Length 108;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
|||||| :| |
Db 22 qgdslrsyytn 32

RESULT 8
AAG62961
ID AAG62961 standard; Protein; 108 AA.
XX
AC AAG62961;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone G101.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42405.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 105; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 108 AA;

Query Match 68.8%; Score 44; DB 22; Length 108;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGDSLRHFYPN 11
|||||| :| |
Db 22 qgdslrsyytn 32

RESULT 9
AAW15559
ID AAW15559 standard; Protein; 109 AA.
XX
AC AAW15559;
XX
DT 27-NOV-1997 (first entry)
XX
DE TGF beta-1/TGF beta-2 cross-reaactive antibody VT37 VL domain.
XX
KW Transforming growth factor beta; TGF-beta; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular didease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy.
XX
OS Homo sapiens.
XX
PN GB2305921-A.
XX
PD 23-APR-1997.
XX
PF 07-OCT-1996; 96GB-0020920.
XX
PR 19-JAN-1996; 96GB-0001081.
PR 06-OCT-1995; 95GB-0020486.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
XX
DR WPI; 1997-215360/20.
DR N-PSDB; AAT60423.
XX
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
XX
PS Example 1; Fig 4; 184pp; English.
XX
CC This polypeptide comprises the VL domain of human scFv antibody
CC VT37, which is cross-reactive with transforming growth factor (TGF)
CC beta-2 and TGF beta-1. It is encoded by a gene (AAT60423) isolated
CC from an scFv repertoire by phage display and soluble ELISA. The
CC dissociation constant of the scFv is 4 nM for TGF beta-1 and 7 nM
CC for TGF beta-2. VT37 does not bind to IGF beta-3. The antigen-
CC binding domains of human antibodies (see also AAW15522-40) to TGF
CC beta-1 and/or beta-2 are useful in the treatment of fibrotic and
CC immune or inflammatory diseases.
XX
SQ Sequence 109 AA;

Query Match 68.8%; Score 44; DB 18; Length 109;

```
  Best Local Similarity   72.7%;  Pred. No. 1.2;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 QGDSLRHFYPN 11
           |||||| :| |
Db      23 qgdslrsyytn 33


RESULT  10
AAU02504
ID   AAU02504 standard; Protein; 109 AA.
XX
AC   AAU02504;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Anti-adipocyte monoclonal antibody light chain, FAT 2.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW   heart disease; complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO200127279-A1.
XX
PD   19-APR-2001.
XX
PF   11-OCT-2000; 2000WO-GB03900.
XX
PR   12-OCT-1999;   99US-0158812.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM,  Main SH,  Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   N-PSDB; AAS03404.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity
PT   related diseases -
XX
PS   Claim 1; Page 96-97; 182pp; English.
XX
CC   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC   sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC   chain, and heavy chain complementarity determining regions (CDR) of the
CC   invention. The antibodies can be used in the treatment of obesity and
CC   obesity related diseases. The antibodies can be used to deliver drugs or
CC   pro-drugs directly to the fat mass of an obese patient or the antibody
CC   can be used as a therapeutic itself. Antibodies binding specifically to
CC   adipocytes can be used to activate the immune system to destroy the cells
CC   by complement mediated lysis. The antibodies may be labeled with a
CC   detectable label such as radiolabel, fluorescent or chemical group and
CC   used in methods of diagnosis in human subjects e.g. to determine the
CC   presence of adipocyte antigen on the surface of an adipocyte to detect or
CC   determine the presence or level of adipocytes in a cell or tissue sample.
CC   The antibodies can be used as an alternative means of treatment for obese
CC   patients other than undergoing surgery to remove excess fat. Antibodies
CC   for different types of fat deposits can also be produced e.g. intra-
CC   abdominal fat associated with heart disease.
XX
SQ   Sequence   109 AA;


  Query Match             68.8%;  Score 44;  DB 22;  Length 109;
  Best Local Similarity   72.7%;  Pred. No. 1.2;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 QGDSLRHFYPN 11
           |||||| :| |
Db      23 qgdslrsyytn 33


RESULT  11
AAR69091
ID   AAR69091 standard; Protein; 109 AA.
XX
AC   AAR69091;
XX
DT   30-AUG-1995  (first entry)
XX
DE   Anti-HIV Fab tat104(VL4).
XX
KW   HIV-1; human immunodeficiency virus type 1; AIDS; Tat protein;
KW   intracellular immunization; gene therapy; single chain antibody;
KW   Fab; antibody engineering; resistance; cell immunity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..20
FT                   /label= FR1
FT   Region          21..31
FT                   /label= CDR1
FT   Region          32..46
FT                   /label= FR2
FT   Region          47..53
FT                   /label= CDR2
FT   Region          54..85
FT                   /label= FR3
FT   Region          86..98
FT                   /label= CDR3
FT   Region          99..109
FT                   /label= FR4
XX
PN   WO9503832-A.
XX
PD   09-FEB-1995.
XX
PF   28-JUL-1994;   94WO-US08448.
XX
PR   30-JUL-1993;   93US-0099870.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Duan L,  Pomerantz R;
XX
DR   WPI; 1995-082039/11.
XX
PT   Method for conducting gene therapy - comprises using recombinant
PT   gene encoding antibody binding antigen associated with a disease;
PT   useful for providing cell immunity.
XX
PS   Example 11; Page 32-33; Table 2; 62pp; English.
XX
CC   A phagemid library was constructed using lymphocyte RNA from
CC   a long-term asymptomatic HIV-1 positive donor.  Heavy and light
CC   chain genes were cloned and a combinatorial library was prepared
CC   and screened to select antigen (HIV rev or tat) binders.  Human
CC   soluble anti-HIV Fabs were obtained.  Heavy chain VH sequences are
CC   given in AAR69084-87, light chain VL in AAR69088-92 and light chain CL
CC   in AAR69093-97.
XX
SQ   Sequence   109 AA;


  Query Match             67.2%;  Score 43;  DB 16;  Length 109;
  Best Local Similarity   72.7%;  Pred. No. 1.9;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 QGDSLRHFYPN 11
           |||||| : | |
Db      21 qgdslryhyan 31
```

```
RESULT  12
AAW08740
ID   AAW08740 standard; Protein; 109 AA.
XX
AC   AAW08740;
XX
DT   08-AUG-1997  (first entry)
XX
DE   Human anti-HIV Fab amino acid sequence tat104(VL4).
XX
KW   Gene therapy; antibody; immunisation; human immunodeficiency virus;
KW   HIV; human T-cell leukaemia virus.
XX
OS   Human Immunodeficiency Virus Type-1.
XX
FH   Key             Location/Qualifiers
FT   Region          1..20
FT                   /label= FR1
FT   Region          21..31
FT                   /label= CDR1
FT   Region          32..46
FT                   /label= FR2
FT   Region          47..53
FT                   /label= CDR2
FT   Region          54..85
FT                   /label= FR3
FT   Region          86..98
FT                   /label= CDR3
FT   Region          99..109
FT                   /label= FR4
XX
PN   WO9637234-A1.
XX
PD   28-NOV-1996.
XX
PF   23-MAY-1996;   96WO-US07393.
XX
PR   23-MAY-1995;   95US-0447610.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Duan L,  Pomerantz RJ;
XX
DR   WPI; 1997-020948/02.
XX
PT   Improved gene therapy using recombinant gene coding for an antibody
PT   - for intracellular immunisation against pathogens recognised by the
PT   antibody, esp. human immunodeficiency virus HIV-1
XX
PS   Example 11; Page 59; 213pp; English.
XX
CC   The present sequence is a human anti-HIV Fab light chain VL sequence.
CC   A novel gene therapy method has been produced, where a recombinant
CC   (rec) gene is introduced into the cells of a mammal. The method is
CC   improved by using a rec gene encoding an antibody (Ab) (e.g. the
CC   present sequence) that is selectively specific for an intracellular
CC   (IC) antigen associated with a disease. The method is used to prevent
CC   or halt the progress of a disease by IC immunisation. Specifically,
CC   the Ab can be used to inhibit the replication of a virus, such as
CC   human T-cell leukaemia virus or especially HIV-1, or of other pathogens,
CC   e.g. bacteria, fungi. The method provides immunity before or after
CC   the development of the disease and can be used to control the
CC   severity of the disease.
XX
SQ   Sequence   109 AA;

  Query Match             67.2%;  Score 43;  DB 18;  Length 109;
  Best Local Similarity   72.7%;  Pred. No. 1.9;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 QGDSLRHFYPN 11
           |||||| : | |
Db     21 qgdslryhyan 31


RESULT  13
AAW21746
ID   AAW21746 standard; protein; 318 AA.
XX
AC   AAW21746;
XX
DT   02-MAR-1998  (first entry)
XX
DE   E3330-binding protein, Ref-1.
XX
KW   E3330-binding protein; Ref-1; microsphere; drug binding factor recovery;
KW   styrene-glycidyl methacrylate polymer; protein isolation;
KW   protein purification; receptor identification.
XX
OS   Synthetic.
XX
PN   EP787988-A2.
XX
PD   06-AUG-1997.
XX
PF   05-FEB-1997;   97EP-0101821.
XX
PR   17-SEP-1996;   96JP-0266711.
PR   05-FEB-1996;   96JP-0018827.
XX
PA   (HAND/) HANDA H.
PA   (KAWA/) KAWAGUCHI H.
XX
PI   Handa H,  Kawaguchi H;
XX
DR   WPI; 1997-387634/36.
XX
PT   Isolation and identification of receptors to specific compounds -
PT   using microspheres prepared by coupling the compound, via a spacer,
PT   to a styrene-glycidyl methacrylate polymer.
XX
PS   Claim 5; Page 11; 29pp; English.
XX
CC   This sequence represents the E3330-binding protein, Ref-1. E3330 is
CC   3-[(5-(2,3-dimethoxy-6-methyl-1,4-benzoquinonyl)]-2-nonyl-2-propionic
CC   acid. This sequence was isolated using the method of the invention. The
CC   method of the invention is for isolating a substance (S1) that can adhere
CC   to a substance (S2) possessing physiological activity from a mixture
CC   containing S1. The method comprises contacting the mixture with a
CC   microsphere prepared by coupling S2 to a styrene-glycidyl methacrylate
CC   polymer through a spacer. The process is useful, e.g., for recovery of
CC   drug binding factors (such as proteins) from cell extracts. The process
CC   allows easy isolation, purification and identification of receptors to
CC   specific compounds.
XX
SQ   Sequence   318 AA;

  Query Match             67.2%;  Score 43;  DB 18;  Length 318;
  Best Local Similarity   77.8%;  Pred. No. 6;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 DSLRHFYPN 11
           || || |||
Db     251 dsfrhlypn 259


RESULT  14
AAW48894
ID   AAW48894 standard; Protein; 318 AA.
XX
AC   AAW48894;
XX
DT   13-OCT-1998  (first entry)
XX
```

DE Homo sapiens AP endonuclease.
XX
KW MGMT; APE; DNA repair protein; fusion protein; AP endonuclease;
KW 0-6-methylguanine-DNA methyltransferase.
XX
OS Homo sapiens.
XX
PN WO9817684-A2.
XX
PD 30-APR-1998.
XX
PF 24-OCT-1997; 97WO-US19629.
XX
PR 25-OCT-1996; 96US-0029308.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Kelley M, Williams D;
XX
DR WPI; 1998-271785/24.
DR N-PSDB; AAV32543.
XX
PT New fusion proteins comprising 2 DNA repair proteins - used for
PT protecting cells against DNA damage, e.g. by chemotherapeutic
PT agents, or for treating DNA-repair-defective human diseases
XX
PS Disclosure; p115-116; 150pp; English.
XX
CC The sequence is that encoding the APE gene which was used in the
CC construction of a fusion protein of the DNA repair
CC proteins 0-6-methylguanine-DNA methyltransferase (MGMT) and AP
CC endonuclease (APE). It can be used for protecting cells
CC (especially bone marrow cells) against DNA damaging agents such as
CC chemotherapeutic agents used in tumour therapy and can be used in
CC conjunction with chemotherapy to facilitate the use of increased doses
CC of chemotherapy. They can provide added protection to cells by
CC providing RPs which recognise different types of DNA lesions. In
CC addition, the FPs can be used in the treatment of DNA-repair-defective
CC human diseases, e.g. Xeroderma Pigmentosum, Ataxia Telangiectasia,
CC Cockayne's syndrome, Bloom's syndrome, Fanconi's anaemia, Parkinson's
CC disease and other neurodegenerative diseases including amyotrophic
CC lateral sclerosis, Alzheimer's disease and other age related disorders.
XX
SQ Sequence 318 AA;

Query Match 67.2%; Score 43; DB 19; Length 318;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSLRHFYPN 11
|| || |||
Db 251 dsfrhlypn 259

RESULT 15
AAW52864
ID AAW52864 standard; Protein; 318 AA.
XX
AC AAW52864;
XX
DT 08-JUL-1998 (first entry)
XX
DE Apurinic/apyrimidinic endonuclease amino acid sequence.
XX
KW Apurinic/apyrimidinic endonuclease; APE; identification; premalignancy;
KW APE level; diagnosis; therapy; tumour; apoptosis.
XX
OS Homo sapiens.
XX
PN WO9747971-A1.
XX
PD 18-DEC-1997.
XX
PF 11-JUN-1997; 97WO-US10078.
XX
PR 11-JUN-1996; 96US-0019602.
PR 11-JUN-1996; 96US-0019561.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Duguid JR, Eble JN, Kelley MR;
XX
DR WPI; 1998-168751/15.
DR N-PSDB; AAV21204.
XX
PT Use of apurinic/apyrimidinic endonuclease - for developing products
PT for the diagnosis and therapy of tumours, or for detecting, inducing
PT or inhibiting apoptosis in cells
XX
PS Disclosure; Pages 131-132; 166pp; English.
XX
CC The present sequence represents an apurinic/apyrimidinic endonuclease
CC (APE). Levels of APE in dysplasia, caicinoma in situ and squamous cell
CC carcinomas of the cervix and prostate are substantially elevated,
CC relative to controls. A method for identifying a premalignant or
CC malignant condition in a human subject comprises determining the
CC level of APE in cells from the subject, where an elevated level of
CC APE, as compared to the APE level in corresponding normal cells,
CC indicates a premalignant or malignant condition. APE levels can be
CC used in the diagnosis and therapy of tumours. They can also be used
CC for detecting, inducing or inhibiting apoptosis in cells, e.g. for
CC treating T-cells infected with HIV or detecting apoptosis in cells
CC that have been subjected to chemo-, radio- or gene therapy.
XX
SQ Sequence 318 AA;

Query Match 67.2%; Score 43; DB 19; Length 318;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSLRHFYPN 11
|| || |||
Db 251 dsfrhlypn 259

Search completed: June 12, 2002, 11:23:33
Job time: 318 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:25:37 ; Search time 61.61 Seconds
(without alignments)
17.156 Million cell updates/sec

Title: US-09-780-035-12
Perfect score: 64
Sequence: 1 QGDSLRHFYPN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	70.3	812	2	H96544	hypothetical prote
2	43	67.2	316	2	S42397	DNA-(apurinic or a
3	43	67.2	317	2	A39500	DNA-(apurinic or a
4	43	67.2	318	2	S23550	DNA-(apurinic or a
5	43	67.2	318	2	S26830	DNA-(apurinic or a
6	41	64.1	165	2	H64460	hypothetical prote
7	41	64.1	452	2	S72266	translation initia
8	41	64.1	1100	2	AF1460	alpha-xylosidase a
9	41	64.1	1100	2	AG1097	alpha-xylosidase a
10	40	62.5	250	2	C71809	exodeoxyribonuclea
11	40	62.5	250	2	F64710	exodeoxyribonuclea
12	40	62.5	332	2	S75928	hypothetical prote
13	40	62.5	368	2	T51200	hypothetical prote
14	39	60.9	96	2	S36060	Ig lambda chain -
15	39	60.9	106	2	S38495	Ig lambda chain -
16	39	60.9	108	2	S38498	Ig lambda chain -
17	39	60.9	108	2	S47184	Ig lambda chain -
18	39	60.9	109	2	S19663	Ig lambda chain V
19	39	60.9	110	2	S36272	Ig lambda chain V
20	39	60.9	115	2	S13726	Ig lambda chain V
21	39	60.9	127	2	S70444	Ig lambda chain pr
22	39	60.9	312	2	G84058	cysteine synthase
23	39	60.9	344	1	YFBSA	phenylalanine--tRN
24	39	60.9	344	2	G84038	phenylalanyl-tRNA
25	39	60.9	370	2	JE0342	E2F transcription
26	38	59.4	98	2	C97777	hypothetical prote
27	38	59.4	233	2	S25748	Ig lambda chain -
28	38	59.4	251	2	AD1669	3'-exo-deoxyribonu
29	38	59.4	251	2	AF1297	3'-exo-deoxyribonu
30	38	59.4	287	2	G83303	probable hydrolase
31	38	59.4	528	2	B96545	hypothetical prote
32	38	59.4	1645	2	AG1897	two-component hybr
33	37	57.8	123	2	T21145	ADP-ribosylation f
34	37	57.8	146	2	S02083	Ig lambda chain V-
35	37	57.8	183	2	T28926	hypothetical prote
36	37	57.8	252	2	S66012	3'-exo-deoxyribonu
37	36	56.2	109	2	S38496	Ig lambda chain -
38	36	56.2	124	2	C82770	hypothetical prote
39	36	56.2	167	2	S67799	hypothetical prote
40	36	56.2	191	2	E70071	conserved hypothet
41	36	56.2	200	2	AD3207	transcription regu
42	36	56.2	226	2	F82052	phosphoglycolate p
43	36	56.2	239	2	C75010	hypothetical prote
44	36	56.2	292	2	S77168	hypothetical prote
45	36	56.2	327	2	AI3308	glutathione S-tran

ALIGNMENTS

RESULT 1
H96544
hypothetical protein F8A12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96544
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H96544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-812 <STO>
A;Cross-references: GB:AE005173; NID:g11094686; PIDN:AAG29622.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8A12.4
A;Map position: 1

Query Match 70.3%; Score 45; DB 2; Length 812;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy       3 DSLRHFYPN 11
           ||| |:|||
Db     371 DSLEHYYPN 379
```

RESULT 2
S42397
DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - rat
N;Alternate names: apurinic/apyrimidinic endonuclease
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 18-Feb-2000
C;Accession: S42397
R;Wilson, T.M.; Carney, J.P.; Kelley, M.R.
Nucleic Acids Res. 22, 530-531, 1994
A;Title: Cloning of the multifunctional rat apurinic/apyrimidinic endonuclease (rAPEN
A;Reference number: S42397; MUID:94173709
A;Accession: S42397
A;Molecule type: mRNA
A;Residues: 1-316 <WIL>
A;Cross-references: GB:L27076; NID:g468370; PIDN:AAA21019.1; PID:g468371
C;Superfamily: exodeoxyribonuclease III

C;Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus

Query Match 67.2%; Score 43; DB 2; Length 316;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSLRHFYPN 11
|| || |||
Db 249 DSFRHLYPN 257

RESULT 3
A39500
DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - mouse
N;Alternate names: apurinic/apyrimidinic endonuclease; desoxyribonuclease
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
C;Accession: A39500; S17524; A56747; I49098; JU0372
R;Seki, S.; Akiyama, K.; Watanabe, S.; Hatsushika, M.; Ikeda, S.; Tsutsui, K.
J. Biol. Chem. 266, 20797-20802, 1991
A;Title: cDNA and deduced amino acid sequence of a mouse DNA repair enzyme (APEX nucleas
A;Reference number: A39500; MUID:92041936
A;Accession: A39500
A;Molecule type: mRNA
A;Residues: 1-317 <SEK>
A;Cross-references: GB:D90374; NID:g220336; PIDN:BAA14382.1; PID:g220337
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Seki, S.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Tsutsui, K.; Akiyama, K.; Zhang, B.
Biochim. Biophys. Acta 1079, 57-64, 1991
A;Title: A mouse DNA repair enzyme (APEX nuclease) having exonuclease and apurinic/apyri
A;Reference number: S17524; MUID:91363416
A;Accession: S17524
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-18,'XXX',22 <SE2>
R;Akiyama, K.; Nagao, K.; Oshida, T.; Tsutsui, K.; Yoshida, M.C.; Seki, S.
Genomics 26, 63-69, 1995
A;Title: Cloning, sequence analysis, and chromosomal assignment of the mouse Apex gene.
A;Reference number: A56747; MUID:95301294
A;Accession: A56747
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <AKI>
A;Cross-references: GB:D38077
R;Takiguchi, Y.; Chen, D.J.
Mamm. Genome 5, 717-722, 1994
A;Title: Genomic structure of the mouse apurinic/apyrimidinic endonuclease gene.
A;Reference number: I49098; MUID:95178846
A;Accession: I49098
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-317 <RES>
A;Cross-references: EMBL:U12273; NID:g533107; PIDN:AAC13769.1; PID:g533108
C;Genetics:
A;Gene: MGI:Apex
A;Cross-references: MGI:88042
A;Introns: 19/1; 81/3; 146/1
C;Superfamily: exodeoxyribonuclease III
C;Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus
F;2-317/Product: DNA repair enzyme APEX nuclease #status experimental <MAT>

Query Match 67.2%; Score 43; DB 2; Length 317;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSLRHFYPN 11
|| || |||
Db 250 DSFRHLYPN 258

RESULT 4

S23550
DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) 1 precursor - human
N;Alternate names: AP endonuclease 1 (APEN); AP1; APEX nuclease; apurinic/apyrimidini
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S23550; S25570; S35454; S35456; S23935; S47521; I39472; S34422; A41631;
R;Xanthoudakis, S.; Miao, G.; Wang, F.; Pan, Y.C.E.; Curran, T.
EMBO J. 11, 3323-3335, 1992
A;Title: Redox activation of Fos-Jun DNA binding activity is mediated by a DNA repair
A;Reference number: S23550; MUID:92371440
A;Accession: S23550
A;Molecule type: mRNA; protein
A;Residues: 1-318 <XAN>
A;Cross-references: GB:S43127; NID:g254068; PIDN:AAB22977.1; PID:g254069
A;Note: part of this sequence, including the amino end of the mature protein, was det
R;Robson, C.N.; Hochhauser, D.; Craig, R.; Rack, K.; Buckle, V.J.; Hickson, I.D.
Nucleic Acids Res. 20, 4417-4421, 1992
A;Title: Structure of the human DNA repair gene HAP1 and its localisation to chromoso
A;Reference number: S25570; MUID:93027134
A;Accession: S25570
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-318 <ROB>
A;Cross-references: EMBL:X66133; NID:g32021; PIDN:CAA46925.1; PID:g32022
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
R;Cheng, X.B.; Bunville, J.; Patterson, T.A.
Nucleic Acids Res. 20, 370, 1992
A;Title: Nucleotide sequence of a cDNA for an apurinic/apyrimidinic endonuclease from
A;Reference number: S35454; MUID:92158631
A;Accession: S35454
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-318 <CHE>
A;Cross-references: EMBL:M81955; NID:g178746; PIDN:AAA58372.1; PID:g178747
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Zhao, B.; Grandy, D.K.; Hagerup, J.M.; Magenis, R.E.; Smith, L.; Chauhan, B.C.; Hen
Nucleic Acids Res. 20, 4097-4098, 1992
A;Title: The human gene for apurinic/apyrimidinic endonuclease (HAP1): sequence and l
A;Reference number: S35456; MUID:92375705
A;Accession: S35456
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <ZHA>
A;Cross-references: EMBL:M92444; NID:g183779; PIDN:AAA58629.1; PID:g183780
R;Seki, S.; Hatsushika, M.; Watanabe, S.; Akiyama, K.; Nagao, K.; Tsutsui, K.
Biochim. Biophys. Acta 1131, 287-299, 1992
A;Title: cDNA cloning, sequencing, expression and possible domain structure of human
A;Reference number: S23935; MUID:92329542
A;Accession: S23935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-50,'H',52-318 <SEK>
A;Cross-references: DDBJ:D13370; NID:g219473; PIDN:BAA02633.1; PID:g219474
R;Akiyama, K.; Seki, S.; Oshida, T.; Yoshida, M.C.
Biochim. Biophys. Acta 1219, 15-25, 1994
A;Title: Structure, promoter analysis and chromosomal assignment of the human APEX ge
A;Reference number: S47521; MUID:94368844
A;Accession: S47521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147,'E',149-318 <AKI>
A;Cross-references: DDBJ:D13370; NID:g219473; PIDN:BAA02633.1; PID:g219474
R;Harrison, L.; Ascione, G.; Menninger, J.C.; Ward, D.C.; Demple, B.
Hum. Mol. Genet. 1, 677-680, 1992
A;Title: Human apurinic endonuclease gene (APE): structure and genomic mapping (chrom
A;Reference number: I39472; MUID:93258307
A;Accession: I39472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <HAR>
A;Cross-references: GB:M99703; NID:g178748; PIDN:AAA58373.1; PID:g553182
R;Robson, C.N.; Hickson, I.D.
Nucleic Acids Res. 19, 5519-5523, 1991

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:39:14 ; Search time 29.47 Seconds
(without alignments)
14.452 Million cell updates/sec

Title: US-09-780-035-12
Perfect score: 64
Sequence: 1 QGDSLRHFYPN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

[redacted] number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	67.2	316	1	APE1_MOUSE	P28352 mus musculu
2	43	67.2	316	1	APE1_RAT	P43138 rattus norv
3	43	67.2	317	1	APE1_BOVIN	P23196 bos taurus
4	43	67.2	317	1	APE1_HUMAN	P27695 homo sapien
5	41	64.1	452	1	E2BG_RAT	P70541 rattus norv
6	39	60.9	344	1	SYFA_BACHD	Q9k895 bacillus ha
7	39	60.9	344	1	SYFA_BACSU	P17921 bacillus su
8	37	57.8	183	1	YS4L_CAEEL	Q01513 caenorhabdi
9	37	57.8	252	1	EXOA_BACSU	P37454 bacillus su
10	37	57.8	318	1	LPSA_BACNO	P39907 bacteroides
11	37	57.8	435	1	XYLA_TETHA	Q82845 tetragenoco
12	37	57.8	874	1	SYV_STRCO	Q06851 streptomyce
13	36	56.2	191	1	YXAF_BACSU	P42105 bacillus su
14	36	56.2	226	1	GPH_VIBCH	Q9knv6 vibrio chol
15	36	56.2	491	1	APM4_YEAST	Q99186 saccharomyc
16	36	56.2	496	1	YKAB_CAEEL	P34262 caenorhabdi
17	36	56.2	621	1	Y708_CHLMU	Q9pjw8 chlamydia m
18	35	54.7	222	1	SFSA_THEAC	Q9hk14 thermoplasm
19	35	54.7	226	1	ATP6_CAPHI	Q32644 capra hircu
20	35	54.7	426	1	CGED_BACSU	P42092 bacillus su
21	35	54.7	439	1	XYLA_LACLA	Q9cfg7 lactococcus
22	35	54.7	439	1	YZ04_METJA	Q60260 methanococc
23	35	54.7	452	1	E2BG_HUMAN	Q9nr50 homo sapien
24	35	54.7	679	1	RRP1_DROME	P27864 drosophila
25	35	54.7	1008	1	VGLM_UUK	P09613 uukuniemi v
26	35	54.7	1628	1	YA8E_SCHPO	Q09779 schizosacch
27	35	54.7	1887	1	RPB1_DROME	P04052 drosophila
28	34	53.1	100	1	HIS1_KLEPN	P05148 klebsiella
29	34	53.1	140	1	YD23_YEAST	Q07549 saccharomyc
30	34	53.1	309	1	UCP2_PIG	O97562 sus scrofa
31	34	53.1	333	1	Y953_PYRAB	Q9uys2 pyrococcus
32	34	53.1	373	1	VGLC_HSVTF	P13374 turkey herp
33	34	53.1	489	1	VGLC_HSVTH	P18535 turkey herp
34	34	53.1	501	1	VGLC_HSVMB	P22650 marek's dis
35	34	53.1	501	1	VGLC_HSVMD	P33500 marek's dis
36	34	53.1	501	1	VGLC_HSVMM	P22651 marek's dis
37	34	53.1	505	1	VGLC_HSVMG	P10681 marek's dis
38	34	53.1	506	1	DNAA_PSEPU	P13454 pseudomonas
39	34	53.1	514	1	DNAA_PSEAE	Q9i7c5 pseudomonas
40	34	53.1	622	1	AMA1_PLAFF	P22621 plasmodium
41	34	53.1	634	1	Y415_HUMAN	O43299 homo sapien
42	34	53.1	685	1	AMY1_DICTH	P09961 dictyoglomu
43	34	53.1	941	1	CHRD_XENLA	Q91713 xenopus lae
44	34	53.1	1320	1	PUR4_NEIMB	Q9jxk5 neisseria m
45	34	53.1	3023	1	POLG_TVMV	P09814 t genome po

ALIGNMENTS

RESULT 1
APE1_MOUSE
ID APE1_MOUSE STANDARD; PRT; 316 AA.
AC P28352;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
DE endonuclease 1) (APEX nuclease) (APEN).
GN APEX OR APE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92041936; PubMed=1939131;
RA Seki S., Akiyama K., Watanabe S., Hatsushika M., Ikeda S.,
RA Tsutsui K.;
RT "cDNA and deduced amino acid sequence of a mouse DNA repair enzyme
RT (APEX nuclease) with significant homology to Escherichia coli
RT exonuclease III.";
RL J. Biol. Chem. 266:20797-20802(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Embryo;
RX MEDLINE=95178846; PubMed=7533013;
RA Takiguchi Y., Chen D.J.;
RT "Genomic structure of the mouse apurinic/apyrimidinic endonuclease
RT gene.";
RL Mamm. Genome 5:717-722(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Blood;
RX MEDLINE=95301294; PubMed=7782087;
RA Akiyama K., Nagao K., Oshida T., Tsutsui K., Yoshida M.C., Seki S.;
RT "Cloning, sequence analysis, and chromosomal assignment of the mouse
RT Apex gene.";
RL Genomics 26:63-69(1995).
RN [4]
RP PARTIAL SEQUENCE OF 1-21, AND CHARACTERIZATION.
RC TISSUE=Ascites;
RX MEDLINE=91363416; PubMed=1716153;
RA Seki S., Ikeda S., Watanabe S., Hatsushika M., Tsutsui K., Akiyama K.,
RA Zhang B.;
RT "A mouse DNA repair enzyme (APEX nuclease) having exonuclease and
RT apurinic/apyrimidinic endonuclease activities: purification and
RT characterization.";
RL Biochim. Biophys. Acta 1079:57-64(1991).
CC -!- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
CC IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
CC REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
CC BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
CC -!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
CC leaving a 3'-terminal unsaturated sugar and a product with a

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CC       terminal 5'-phosphate.
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90374; BAA14382.1; -.
DR   EMBL; U12273; AAC13769.1; -.
DR   EMBL; D38077; BAA07270.1; -.
DR   PIR; S17524; S17524.
DR   PIR; A39500; A39500.
DR   HSSP; P27695; 1BIX.
DR   MGD; MGI:88042; Apex.
DR   InterPro; IPR000097; AP_endonclse_family_1.
DR   Pfam; PF01260; AP_endonucleas1; 1.
DR   PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR   PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR   PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW   DNA repair; Lyase; Nuclear protein.
FT   INIT_MET      0      0
FT   METAL        66     66       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL        94     94       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL       208    208       MAGNESIUM OR MANGANESE (BY SIMILARITY).
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FT   METAL       307    307       MAGNESIUM OR MANGANESE (BY SIMILARITY).
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FT                                 SIMILARITY).
FT   ACT_SITE    307    307       GENERAL BASE (BY SIMILARITY).
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  Query Match             67.2%;  Score 43;  DB 1;  Length 316;
  Best Local Similarity   77.8%;  Pred. No. 1.2;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 DSLRHFYPN 11
           || || |||
Db     249 DSFRHLYPN 257


ULT   2
1_RAT
ID   APE1_RAT       STANDARD;      PRT;   316 AA.
AC   P43138;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
DE   endonuclease 1) (APEX nuclease) (APEN).
GN   APEX OR APE.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX   MEDLINE=94173709; PubMed=7510394;
RA   Wilson T.M., Carney J.P., Kelley M.R.;
RT   "Cloning of the multifunctional rat apurinic/apyrimidinic
RT   endonuclease (rAPEN)/redox factor from an immature T cell line.";
RL   Nucleic Acids Res. 22:530-531(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA   Tan Y., Akiyama K., Seki S., Tabayashi T., Taniyama M.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yao M., Akiyama K., Tan Y., Sarker A.H., Ikeda S., Alam S.S.,
RA   Tsutsui K., Yoshida M.C., Seki S.;
RT   "Genomic structure of the rat Apex (major AP endonuclease) gene with
RT   an adjacent putative O-sialoglycoprotease (Prsmg1/Gcp11) gene and a
RT   processed pseudogene (Apexp1).";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
CC       IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
CC       REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
CC       BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
CC   -!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
CC       apyrimidinic site in DNA is broken by a beta-elimination reaction,
CC       leaving a 3'-terminal unsaturated sugar and a product with a
CC       terminal 5'-phosphate.
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear..
CC   -!- SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L27076; AAA21019.1; -.
DR   EMBL; D44495; BAA07938.1; -.
DR   EMBL; AB023065; BAA82124.1; -.
DR   HSSP; P27695; 1BIX.
DR   InterPro; IPR000097; AP_endonclse_family_1.
DR   Pfam; PF01260; AP_endonucleas1; 1.
DR   PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR   PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR   PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW   DNA repair; Lyase; Nuclear protein.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   METAL        66     66       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL        94     94       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL       208    208       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL       210    210       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL       306    306       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   METAL       307    307       MAGNESIUM OR MANGANESE (BY SIMILARITY).
FT   ACT_SITE    307    307       GENERAL BASE (BY SIMILARITY).
FT   CONFLICT      9      9       MISSING (IN REF. 1).
FT   CONFLICT    235    235       R -> A (IN REF. 1).
FT   CONFLICT    287    287       H -> Q (IN REF. 1).
SQ   SEQUENCE   316 AA;  35407 MW;  FB27D005917C4116 CRC64;


  Query Match             67.2%;  Score 43;  DB 1;  Length 316;
  Best Local Similarity   77.8%;  Pred. No. 1.2;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 DSLRHFYPN 11
           || || |||
Db     249 DSFRHLYPN 257


RESULT   3
APE1_BOVIN
ID   APE1_BOVIN      STANDARD;      PRT;   317 AA.
AC   P23196;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
DE   endonuclease 1) (APEX nuclease) (APEN).
GN   APEX OR APE OR BAP1.
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:38:40 ; Search time 107.96 Seconds
(without alignments)
17.626 Million cell updates/sec

Title: US-09-780-035-12
Perfect score: 64
Sequence: 1 QGDSLRHFYPN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	70.3	812	10	Q9C6J9	Q9c6j9 arabidopsis
2	43	67.2	289	11	Q99PF3	Q99pf3 rattus norv
3	43	67.2	317	11	Q9Z2J2	Q9z2j2 cricetulus
4	43	67.2	318	4	Q969L5	Q96915 homo sapien
5	42	65.6	616	5	Q95RL0	Q95rl0 drosophila
6	41	64.1	165	17	Q58685	Q58685 methanococc
7	41	64.1	177	10	Q9SM57	Q9sm57 pisum sativ
8	41	64.1	1100	16	Q92F85	Q92f85 listeria in
9	40	62.5	60	5	Q9BJJ1	Q9bjj1 plasmodium
10	40	62.5	179	5	Q9U7J9	Q9u7j9 plasmodium
11	40	62.5	250	16	O26054	O26054 helicobacte
12	40	62.5	250	16	Q9ZJ98	Q9zj98 helicobacte
13	40	62.5	332	16	P74293	P74293 synechocyst
14	40	62.5	902	3	Q96U03	Q96u03 neurospora
15	40	62.5	2163	5	Q9NFB6	Q9nfb6 plasmodium
16	39	60.9	107	4	Q9NSD6	Q9nsd6 homo sapien
17	39	60.9	312	16	Q9K7T8	Q9k7t8 bacillus ha
18	39	60.9	370	5	O77051	O77051 drosophila
19	38	59.4	98	16	Q92I01	Q92i01 rickettsia
20	38	59.4	251	16	Q92AM6	Q92am6 listeria in
21	38	59.4	287	16	Q9I098	Q9i098 pseudomonas
22	38	59.4	349	4	Q9H7J1	Q9h7j1 homo sapien
23	38	59.4	528	10	Q9C6J7	Q9c6j7 arabidopsis
24	38	59.4	1148	4	Q9H7S7	Q9h7s7 homo sapien
25	38	59.4	1890	4	Q96RK2	Q96rk2 homo sapien
26	37	57.8	123	5	Q93536	Q93536 caenorhabdi
27	37	57.8	261	5	Q9N9X0	Q9n9x0 giardia lam
28	37	57.8	362	5	Q95W41	Q95w41 branchiosto
29	37	57.8	379	4	Q9NWS4	Q9nws4 homo sapien
30	37	57.8	427	16	Q9CLD3	Q9cld3 pasteurella
31	37	57.8	502	4	Q9P233	Q9p233 homo sapien
32	36	56.2	124	16	Q9PFE3	Q9pfe3 xylella fas
33	36	56.2	167	3	Q07688	Q07688 saccharomyc
34	36	56.2	239	17	Q9UY91	Q9uy91 pyrococcus
35	36	56.2	292	16	P73680	P73680 synechocyst
36	36	56.2	319	4	Q9H6U2	Q9h6u2 homo sapien
37	36	56.2	344	16	O25127	O25127 helicobacte
38	36	56.2	367	2	Q45125	Q45125 bacteroides
39	36	56.2	447	2	Q9X6D1	Q9x6d1 thermus the
40	36	56.2	624	17	Q9HSH3	Q9hsh3 halobacteri
41	36	56.2	681	16	Q99X32	Q99x32 staphylococ
42	36	56.2	715	5	Q9VVD2	Q9vvd2 drosophila
43	36	56.2	830	16	Q9KGI3	Q9kgi3 bacillus ha
44	36	56.2	1028	10	Q9C7J0	Q9c7j0 arabidopsis
45	35.5	55.5	1134	5	Q21554	Q21554 caenorhabdi

ALIGNMENTS

RESULT 1
Q9C6J9
ID Q9C6J9 PRELIMINARY; PRT; 812 AA.
AC Q9C6J9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 91.5 KDA PROTEIN.
GN F8A12.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL; AC079284; AAG50928.1; -.
KW Hypothetical protein.

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SQ   SEQUENCE   812 AA;  91486 MW;  A45C45BA40056679 CRC64;


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  Best Local Similarity   77.8%;  Pred. No. 6.7;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 DSLRHFYPN 11
          ||| |:|||
Db    371 DSLEHYYPN 379


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ID   Q99PF3      PRELIMINARY;      PRT;   289 AA.
AC   Q99PF3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   APEX (FRAGMENT).
GN   APEX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NORWAY;
RA   Xie Z.H., Liu C.Z., He Y.H., Wang A.M., Ma C.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF311054; AAG49922.1; -.
DR   HSSP; P27695; 1BIX.
DR   InterPro; IPR000097; AP_endonclse_family_1.
DR   Pfam; PF01260; AP_endonucleas1; 2.
DR   PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR   PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR   PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   289 AA;  32353 MW;  67E82454D062CE51 CRC64;


  Query Match             67.2%;  Score 43;  DB 11;  Length 289;
  Best Local Similarity   77.8%;  Pred. No. 5.3;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 DSLRHFYPN 11
          || || |||
Db    222 DSFRHLYPN 230


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AC   Q9Z2J2;
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DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   APURINIC/APYRIMIDINIC ENDONUCLEASE.
GN   APE.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY;
RX   MEDLINE=20075118; PubMed=10606812;
RA   Purohit S., Arenaz P.;
RT   "Molecular cloning, sequence and structure analysis of hamster
RT   apurinic/apyrimidinic endonuclease (chAPE1) gene.";
RL   Mutat. Res. 435:215-224(1999).
DR   EMBL; AF056934; AAD02702.1; -.
DR   HSSP; P27695; 1E9N.
DR   InterPro; IPR000097; AP_endonclse_family_1.
DR   Pfam; PF01260; AP_endonucleas1; 1.
DR   PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
DR   PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
DR   PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
KW   Endonuclease.
SQ   SEQUENCE   317 AA;  35512 MW;  76DD6F3975455408 CRC64;


  Query Match             67.2%;  Score 43;  DB 11;  Length 317;
  Best Local Similarity   77.8%;  Pred. No. 5.9;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 DSLRHFYPN 11
          || || |||
Db    250 DSFRHLYPN 258


RESULT   4
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ID   Q969L5      PRELIMINARY;      PRT;   318 AA.
AC   Q969L5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   APEX NUCLEASE (MULTIFUNCTIONAL DNA REPAIR ENZYME).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG CARCINOMA;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008145; AAH08145.1; -.
DR   EMBL; BC002338; AAH02338.1; -.
SQ   SEQUENCE   318 AA;  35568 MW;  B943A23BF487B5D3 CRC64;


  Query Match             67.2%;  Score 43;  DB 4;  Length 318;
  Best Local Similarity   77.8%;  Pred. No. 5.9;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 DSLRHFYPN 11
          || || |||
Db    251 DSFRHLYPN 259


RESULT   5
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ID   Q95RL0      PRELIMINARY;      PRT;   616 AA.
AC   Q95RL0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LD21694P.
GN   CG2980.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:28 ; Search time 49.09 Seconds
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5.473 Million cell updates/sec

Title: US-09-780-035-12
Perfect score: 64
Sequence: 1 QGDSLRHFYPN 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	67.2	318	2	US-08-872-719-2	Sequence 2, Appli
2	43	67.2	318	3	US-08-957-302A-12	Sequence 12, Appl
3	43	67.2	318	4	US-09-336-890-2	Sequence 2, Appli
4	43	67.2	318	4	US-09-542-403-12	Sequence 12, Appl
5	43	67.2	319	2	US-08-795-927-4	Sequence 4, Appli
6	43	67.2	524	3	US-08-957-302A-2	Sequence 2, Appli
7	43	67.2	524	4	US-09-542-403-2	Sequence 2, Appli
8	39	60.9	97	2	US-08-665-202-35	Sequence 35, Appl
9	39	60.9	103	2	US-08-273-146-71	Sequence 71, Appl
10	39	60.9	104	4	US-09-240-274-49	Sequence 49, Appl
11	39	60.9	106	4	US-09-240-274-50	Sequence 50, Appl
12	39	60.9	109	2	US-08-652-816A-16	Sequence 16, Appl
13	39	60.9	109	2	US-08-665-202-34	Sequence 34, Appl
14	39	60.9	278	4	US-09-260-527-3	Sequence 3, Appli
15	39	60.9	280	4	US-09-260-527-1	Sequence 1, Appli
16	39	60.9	309	4	US-09-079-029-9	Sequence 9, Appli
17	39	60.9	312	4	US-09-079-029-10	Sequence 10, Appl
18	38	59.4	104	4	US-08-793-450-2	Sequence 2, Appli
19	38	59.4	238	4	US-08-793-450-6	Sequence 6, Appli
20	35	54.7	106	4	US-09-240-274-47	Sequence 47, Appl
21	35	54.7	106	4	US-09-240-274-48	Sequence 48, Appl
22	35	54.7	352	1	US-08-785-052-2	Sequence 2, Appli
23	35	54.7	352	2	US-08-913-581-2	Sequence 2, Appli
24	35	54.7	439	1	US-07-637-870-9	Sequence 9, Appli
25	35	54.7	439	1	US-07-637-399-6	Sequence 6, Appli
26	35	54.7	439	1	US-08-112-703-6	Sequence 6, Appli
27	34	53.1	250	4	US-09-036-987A-9	Sequence 9, Appli
28	34	53.1	250	4	US-09-370-700-9	Sequence 9, Appli
29	34	53.1	489	2	US-08-663-566A-6	Sequence 6, Appli
30	34	53.1	489	2	US-08-023-610-6	Sequence 6, Appli
31	34	53.1	489	2	US-08-288-065A-6	Sequence 6, Appli
32	34	53.1	489	2	US-08-362-240A-6	Sequence 6, Appli
33	34	53.1	489	4	US-08-804-372A-4	Sequence 4, Appli
34	34	53.1	489	5	PCT-US95-10245-6	Sequence 6, Appli
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37	34	53.1	501	2	US-08-288-065A-9	Sequence 9, Appli
38	34	53.1	501	2	US-08-362-240A-9	Sequence 9, Appli
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41	34	53.1	628	1	US-08-257-073-9	Sequence 9, Appli
42	34	53.1	940	2	US-08-938-365-4	Sequence 4, Appli
43	34	53.1	941	1	US-08-343-760A-2	Sequence 2, Appli
44	33	51.6	366	1	US-08-700-359-22	Sequence 22, Appl
45	33	51.6	378	2	US-08-401-068-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-872-719-2
; Sequence 2, Application US/08872719
; Patent No. 5919643
; GENERAL INFORMATION:
; APPLICANT: Kelley, Mark R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE USE OF APURINIC/APYRIMIDIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77057-2198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,719
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: INDY:012PZ1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-872-719-2

Query Match 67.2%; Score 43; DB 2; Length 318;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       3 DSLRHFYPN 11
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Db     251 DSFRHLYPN 259
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RESULT 2

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US-08-957-302A-12
; Sequence 12, Application US/08957302A
; Patent No. 6046036
;  GENERAL INFORMATION:
;    APPLICANT:  Kelley, Mark
;    APPLICANT:  Williams, David
;    TITLE OF INVENTION:  DNA Sequences Encoding Fusions of DNA
;    TITLE OF INVENTION:  Repair Proteins and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/957,302A
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  INDY:005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-957-302A-12


  Query Match             67.2%;  Score 43;  DB 3;  Length 318;
  Best Local Similarity   77.8%;  Pred. No. 2.9;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 DSLRHFYPN 11
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Db     251 DSFRHLYPN 259


RESULT   3
US-09-336-890-2
; Sequence 2, Application US/09336890
; Patent No. 6190661
;  GENERAL INFORMATION:
;    APPLICANT:  Kelley, Mark R.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR THE USE OF
;    TITLE OF INVENTION:  APURINIC/APYRIMIDINIC
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77057-2198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;      APPLICATION NUMBER:  US/09/336,890
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/872,719
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  INDY:012PZ1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-09-336-890-2


  Query Match             67.2%;  Score 43;  DB 4;  Length 318;
  Best Local Similarity   77.8%;  Pred. No. 2.9;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 DSLRHFYPN 11
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Db     251 DSFRHLYPN 259


RESULT   4
US-09-542-403-12
; Sequence 12, Application US/09542403
; Patent No. 6252048
;  GENERAL INFORMATION:
;    APPLICANT:  Kelley, Mark
;    APPLICANT:  Williams, David
;    TITLE OF INVENTION:  DNA Sequences Encoding Fusions of DNA
;    TITLE OF INVENTION:  Repair Proteins and Uses Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/542,403
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/957,302
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  INDY:005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-09-542-403-12
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:33 ; Search time 136.11 Seconds
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5.712 Million cell updates/sec

Title: US-09-780-035-13
Perfect score: 39
Sequence: 1 GKNNRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	7	21	AAY95196	Anti-platelet glyc
2	39	100.0	7	21	AAY95217	Anti-platelet glyc
3	39	100.0	7	22	AAG65303	Anti-IL-18 antibod
4	39	100.0	67	16	AAR80089	Human derived ligh
5	39	100.0	67	20	AAW95487	Human-derived RT3
6	39	100.0	101	13	AAR22572	Light chain VL3.5
7	39	100.0	103	16	AAR80091	Human derived ligh
8	39	100.0	103	20	AAW95489	Human-derived RT3
9	39	100.0	104	17	AAR93164	Anti-rhesus D mono
10	39	100.0	106	22	AAU02518	Anti-adipocyte mon
11	39	100.0	106	22	AAU02531	Anti-adipocyte mon
12	39	100.0	107	16	AAR69092	Anti-HIV Fab tat10
13	39	100.0	107	18	AAW15528	Anti-TGF beta-2 sc
14	39	100.0	107	18	AAW08741	Human anti-HIV Fab
15	39	100.0	107	21	AAY95194	Anti-platelet glyc
16	39	100.0	107	21	AAY95215	Anti-platelet glyc
17	39	100.0	107	22	AAG62969	Amino acid sequenc
18	39	100.0	108	21	AAY95179	Anti-platelet glyc
19	39	100.0	108	21	AAY95185	Anti-platelet glyc
20	39	100.0	108	21	AAY44616	Human antibody clo
21	39	100.0	108	22	AAG62939	Amino acid sequenc
22	39	100.0	109	18	AAW19884	CEA-specific antib
23	39	100.0	109	18	AAW15525	Anti-TGF beta-2 sc
24	39	100.0	109	18	AAW08583	Human antibody C4.
25	39	100.0	109	19	AAW47181	Variable light (VL
26	39	100.0	109	19	AAW47182	Variable light (VL
27	39	100.0	109	22	AAU02509	Anti-adipocyte mon
28	39	100.0	109	22	AAU02513	Anti-adipocyte mon
29	39	100.0	109	22	AAG65309	Anti-IL-18 antibod
30	39	100.0	109	22	AAG65353	Anti-IL-18 antibod
31	39	100.0	110	18	AAW15526	Anti-TGF beta-2 sc
32	39	100.0	111	21	AAY99559	Human LH13 monoclo
33	39	100.0	115	22	AAG65557	Amino acid sequenc
34	39	100.0	115	22	AAG65559	Amino acid sequenc
35	39	100.0	125	21	AAY65088	Human 5' EST relat
36	39	100.0	229	19	AAW49694	Human ScFv5 agains
37	39	100.0	236	19	AAW49690	Human ScFv1 agains
38	39	100.0	236	22	AAB46055	Human TF anti-idio
39	39	100.0	237	19	AAW49691	Human ScFv2 agains
40	39	100.0	237	21	AAY95219	Anti-platelet glyc
41	39	100.0	238	17	AAR93165	Anti-rhesus D reco
42	39	100.0	238	21	AAY95198	Anti-platelet glyc
43	39	100.0	239	19	AAW49692	Human ScFv3 agains
44	39	100.0	239	22	AAB46054	Human TF anti-idio
45	39	100.0	240	22	AAB46052	Human TF anti-idio

ALIGNMENTS

RESULT 1
AAY95196
ID AAY95196 standard; Peptide; 7 AA.
XX
AC AAY95196;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-1 VL CDR2.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-1;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -

XX
PS Claim 20; Fig 5; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 2 (CDR2) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-1 (see AAY95198), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 39; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 1 gknnrps 7

RESULT 2
AAY95217
ID AAY95217 standard; Peptide; 7 AA.
XX
AC AAY95217;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-3 VL CDR2.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-3;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Claim 20; Fig 7; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 2 (CDR2) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-3 (see AAY95219), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 39; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 1 gknnrps 7

RESULT 3
AAG65303
ID AAG65303 standard; protein; 7 AA.
XX
AC AAG65303;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR2 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 27; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a

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CC   disorder where IL-18 is detrimental in, a human subject suffering from,
CC   inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC   inflammatory bowel disease, and osteoarthritis), neurological disorders
CC   (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC   stroke), heart failure, myocardial infarction, autoimmune diseases such
CC   as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC   (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC   antibody may occur before, concurrent, or after administration of a
CC   second agent selected from an antibody, or fragment, capable of binding
CC   human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC   cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC   agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC   chain CDR2 fragment.
XX
SQ   Sequence   7 AA;


  Query Match             100.0%;  Score 39;  DB 22;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db      1 gknnrps 7


RESULT   4
AAR80089
ID   AAR80089 standard; Protein; 67 AA.
XX
AC   AAR80089;
XX
DT   23-MAY-1996  (first entry)
XX
DE   Human derived light chain RT3 phage antibody.
XX
KW   Light chain; RT3; human; catalytic antibody; bacteriophage.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          2..5
FT                   /note= "framework region 2"
FT   Region          6..12
FT                   /note= "complementarity determining region 2"
FT   Region          13..44
FT                   /note= "framework region 3"
FT   Region          45..56
FT                   /note= "complementarity determining region 3"
FT   Region          57..67
FT                   /note= "framework region 4"
XX
PN   WO9527045-A1.
XX
PD   12-OCT-1995.
XX
PF   30-MAR-1994;   94WO-US03420.
XX
PR   30-MAR-1994;   94WO-US03420.
XX
PA   (IGEN-) IGEN INC.
XX
PI   Chiswell D,  Darsley MJ,  Fitzgerald K,  Kenten JH;
PI   Martin MT,  McCafferty J,  Smith RG,  Titmas RC,  Williams RO;
XX
DR   WPI; 1995-358624/46.
DR   N-PSDB; AAT04636.
XX
PT   Production of catalytic antibodies displayed on phage - by
PT   generating a gene library of antibody-derived domains and expressing
PT   it in phage vectors
XX
PS   Disclosure; Fig 20; 133pp; English.
XX
CC   AAT04636 encodes AAR80089 human derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody (CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. in vivo.
XX
SQ   Sequence   67 AA;


  Query Match             100.0%;  Score 39;  DB 16;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db      6 gknnrps 12


RESULT   5
AAW95487
ID   AAW95487 standard; Protein; 67 AA.
XX
AC   AAW95487;
XX
DT   29-MAR-1999  (first entry)
XX
DE   Human-derived RT3 phage antibody light chain genetic sequence.
XX
KW   Catalytic; antibody; phage display; immunising; phage expression vector;
KW   prodrug; scFV; RT3.
XX
OS   Homo sapiens.
XX
PN   US5855885-A.
XX
PD   05-JAN-1999.
XX
PF   14-JUL-1994;   94US-0273146.
XX
PR   22-JAN-1993;   93US-0007684.
PR   14-JUL-1994;   94US-0273146.
XX
PA   (CHIS/) CHISWELL D.
PA   (DARS/) DARSLEY M J.
PA   (FITZ/) FITZGERALD K.
PA   (KENT/) KENTEN J H.
PA   (MART/) MARTIN M T.
PA   (MCCA/) MCCAFFERTY J.
PA   (SMIT/) SMITH R.
PA   (TITM/) TITMAS R C.
PA   (WILL/) WILLIAMS R O.
XX
PI   Chiswell D,  Darsley MJ,  Fitzgerald K,  Kenten JH;
PI   Martin MT,  McCafferty J,  Smith R,  Titmas RC,  Williams RO;
XX
DR   WPI; 1999-105036/09.
DR   N-PSDB; AAX00886.
XX
PT   Production of catalytic antibodies displayed on bacteriophages -
PT   comprises generating a gene library of antibody-derived domains
PT   inserting coding into a phage expression vector and isolating the
PT   catalytic antibodies
XX
PS   Examples; Fig 20D; 117pp; English.
XX
CC   The invention relates to methods for producing catalytic antibodies
CC   displayed on a phage. The method comprises: (a) generating a gene
CC   library of antibody-derived domains; (b) inserting coding for the domains
CC   into a phage expression vector; and (c) isolating the catalytic
CC   antibodies. The phage expression vector incorporates a histidine peptide
CC   in tandem with a myc peptide. The catalytic antibodies can be isolated by
CC   preparing an antigen; optionally immunising an animal with the antigen;
```

CC generating a library of VH and VL domains from the immunised animal;
CC cloning the VH and VL domains into a phage expression vector to generate
CC phage display antibodies; selecting phage display antibodies which bind
CC specifically to the antigen; screening the selected phage display
CC antibodies for catalytic activity to substrate; and isolating the
CC catalytic antibodies, where the phage expression vector incorporates a
CC histidine peptide in tandem with a myc peptide. The processes are used to
CC produce catalytic antibodies, which can be used for in vivo activation of
CC a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy
CC and light chains of RT3 specific phage antibodies selected from a naive
CC human phage antibody library.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 39; DB 20; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
6 gknnrps 12

RESULT 6
AAR22572
ID AAR22572 standard; Protein; 101 AA.
XX
AC AAR22572;
XX
DT 21-MAY-1992 (first entry)
XX
DE Light chain VL3.5 from BSA binding scFv fragment.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; human.
XX
OS Homo sapiens.
XX
PN WO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
XX
DR WPI; 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Table 11; Page 152; 109pp; English.
XX
CC PCR was used to prepare a human scFv library from RNA from white
CC blood cells from an unimmunised donor. Heavy chains from IgG and
CC IgM antibodies were amplified separately. Four separate libraries
CC were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
CC purified scFv fragments were ligated into the phagemid pHEN1 for
CC expression on the surface of fd bacteriophage as gene III fusions.
CC The clones were then subjected to affinity selection for binding
CC to phOx:BSA by selection on tubes followed by analysis by ELISA. Of
CC 96 clones analysed, 43 showed binding to both phOx:BSA and BSA.
CC These were designated BSA binders. Thirteen of fourteen clones
CC sequenced had the same sequence, the VH derived from a human VH3
CC family gene (AAR22571) and the VL from a human V lambda 3 family
CC gene (shown here). The other was derived from a human VH4 family
CC gene and a human Vk1 family gene. One clone bound only to phOx:BSA
CC (oxazolone binder). This sequence revealed a VH derived from a
CC human VH1 family gene (AAR22569) and VL from a human V lambda 1
CC family gene (AAR22570).
CC See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
XX
SQ Sequence 101 AA;

Query Match 100.0%; Score 39; DB 13; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 49 gknnrps 55

RESULT 7
AAR80091
ID AAR80091 standard; Protein; 103 AA.
XX
AC AAR80091;
XX
DT 23-MAY-1996 (first entry)
XX
DE Human derived light chain RT3 phage antibody.
XX
KW Light chain; RT3; human; catalytic antibody; bacteriophage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..16
FT /note= "framework region 1"
FT Region 17..27
FT /note= "complimentarity determining region 1"
FT Region 28..43
FT /note= "framework region 2"
FT Region 44..49
FT /note= "complementarity determining region 2"
FT Region 50..82
FT /note= "framework region 3"
FT Region 83..92
FT /note= "complementarity determining region 3"
FT Region 93..103
FT /note= "framework region 4"
XX
PN WO9527045-A1.
XX
PD 12-OCT-1995.
XX
PF 30-MAR-1994; 94WO-US03420.
XX
PR 30-MAR-1994; 94WO-US03420.
XX
PA (IGEN-) IGEN INC.
XX
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
XX
DR WPI; 1995-358624/46.
DR N-PSDB; AAT04638.
XX
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing

```
PT   it in phage vectors
XX
PS   Disclosure; Fig 20; 133pp; English.
XX
CC   AAT04638 encodes AAR80091 human derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody (CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. in vivo.
XX
SQ   Sequence   103 AA;


  Query Match             100.0%;  Score 39;  DB 16;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      43 gknnrps 49


RESULT   8
AAW95489
ID   AAW95489 standard; Protein; 103 AA.
XX
AC   AAW95489;
XX
DT   29-MAR-1999  (first entry)
XX
DE   Human-derived RT3 phage antibody light chain genetic sequence.
XX
KW   Catalytic; antibody; phage display; immunising; phage expression vector;
KW   prodrug; scFV; RT3.
XX
OS   Homo sapiens.
XX
PN   US5855885-A.
XX
PD   05-JAN-1999.
XX
PF   14-JUL-1994;   94US-0273146.
XX
PR   22-JAN-1993;   93US-0007684.
PR   14-JUL-1994;   94US-0273146.
XX
PA   (CHIS/) CHISWELL D.
PA   (DARS/) DARSLEY M J.
PA   (FITZ/) FITZGERALD K.
PA   (KENT/) KENTEN J H.
PA   (MART/) MARTIN M T.
PA   (MCCA/) MCCAFFERTY J.
PA   (SMIT/) SMITH R.
PA   (TITM/) TITMAS R C.
PA   (WILL/) WILLIAMS R O.
XX
PI   Chiswell D,  Darsley MJ,  Fitzgerald K,  Kenten JH;
PI   Martin MT,  McCafferty J,  Smith R,  Titmas RC,  Williams RO;
XX
DR   WPI; 1999-105036/09.
DR   N-PSDB; AAX00888.
XX
PT   Production of catalytic antibodies displayed on bacteriophages -
PT   comprises generating a gene library of antibody-derived domains
PT   inserting coding into a phage expression vector and isolating the
PT   catalytic antibodies
XX
PS   Examples; Fig 20F; 117pp; English.
XX
CC   The invention relates to methods for producing catalytic antibodies
CC   displayed on a phage. The method comprises: (a) generating a gene
CC   library of antibody-derived domains; (b) inserting coding for the domains
CC   into a phage expression vector; and (c) isolating the catalytic
CC   antibodies. The phage expression vector incorporates a histidine peptide
CC   in tandem with a myc peptide. The catalytic antibodies can be isolated by
CC   preparing an antigen; optionally immunising an animal with the antigen;
CC   generating a library of VH and VL domains from the immunised animal;
CC   cloning the VH and VL domains into a phage expression vector to generate
CC   phage display antibodies; selecting phage display antibodies which bind
CC   specifically to the antigen; screening the selected phage display
CC   antibodies for catalytic activity to substrate; and isolating the
CC   catalytic antibodies, where the phage expression vector incorporates a
CC   histidine peptide in tandem with a myc peptide. The processes are used to
CC   produce catalytic antibodies, which can be used for in vivo activation of
CC   a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy
CC   and light chains of RT3 specific phage antibodies selected from a naive
CC   human phage antibody library.
XX
SQ   Sequence   103 AA;


  Query Match             100.0%;  Score 39;  DB 20;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      43 gknnrps 49


RESULT   9
AAR93164
ID   AAR93164 standard; Protein; 104 AA.
XX
AC   AAR93164;
XX
DT   29-OCT-1996  (first entry)
XX
DE   Anti-rhesus D monoclonal antibody D7C2 light chain V region.
XX
KW   Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW   rhesus positive; rhesus negative; haemolysis; lambda light chain;
KW   variable region; insect host cell; baculovirus; recombinant production.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          23..33
FT                   /label= CDR1
FT                   /note= "complementarity determining region"
FT   Region          49..55
FT                   /label= CDR2
FT                   /note= "complementarity determining region"
FT   Region          88..93
FT                   /label= CDR3
FT                   /note= "complementarity determining region"
XX
PN   FR2724182-A1.
XX
PD   08-MAR-1996.
XX
PF   02-SEP-1994;   94FR-0010566.
XX
PR   02-SEP-1994;   94FR-0010566.
XX
PA   (INSP ) INST PASTEUR.
PA   (PROT-) PROTEINE PERFORMANCE.
XX
PI   Chaabihi H,  Edelman L,  Kaczorek M,  Margaritte C;
XX
DR   WPI; 1996-162018/17.
DR   N-PSDB; AAT26869.
XX
PT   Recombinant anti-rhesus D monoclonal antibody - expressed by
PT   baculovirus-transformed insect cells and useful for preventing
PT   haemolysis in new-born babies
```

XX
PS Example 1; Page 30; 46pp; French.
XX
CC The human monoclonal antibody D7C2, of isotype IgM, recognises a
CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
CC cells. The antibody agglutinates rhesus positive cells but not
CC rhesus negative cells and is useful diagnostically and also for
CC preventing haemolysis in new-born rhesus positive babies.
CC Recombinant IgM-D7C2 can be produced by insect cells which have
CC been transformed by a baculoviral vector comprising a D7C2
CC expression cassette. The present sequence is that of the variable
CC region of the IgM-D7C2 light chain.
XX
SQ Sequence 104 AA;

Query Match 100.0%; Score 39; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 49 gknnrps 55

RESULT 10
AAU02518
ID AAU02518 standard; Protein; 106 AA.
XX
AC AAU02518;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 11.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03418.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS Claim 1; Page 104; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 39; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 49 gknnrps 55

RESULT 11
AAU02531
ID AAU02531 standard; Protein; 106 AA.
XX
AC AAU02531;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 20.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03431.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS Claim 1; Page 112; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 106 AA;

```
  Query Match             100.0%;  Score 39;  DB 22;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      49 gknnrps 55


RESULT  12
AAR69092
ID   AAR69092 standard; Protein; 107 AA.
XX
AC   AAR69092;
XX
DT   30-AUG-1995  (first entry)
XX
DE   Anti-HIV Fab tat107(VL4).
XX
KW   HIV-1; human immunodeficiency virus type 1; AIDS; Tat protein;
KW   intracellular immunization; gene therapy; single chain antibody;
KW   Fab; antibody engineering; resistance; cell immunity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..20
FT                   /label= FR1
FT   Region          21..31
FT                   /label= CDR1
FT   Misc-difference 27
FT                   /note= "not known"
FT   Region          32..46
FT                   /label= FR2
FT   Region          47..53
FT                   /label= CDR2
FT   Region          54..85
FT                   /label= FR3
FT   Region          86..96
FT                   /label= CDR3
FT   Region          97..107
FT                   /label= FR4
XX
PN   WO9503832-A.
XX
PD   09-FEB-1995.
XX
PR   28-JUL-1994;   94WO-US08448.
XX
PR   30-JUL-1993;   93US-0099870.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Duan L,  Pomerantz R;
XX
DR   WPI; 1995-082039/11.
XX
PT   Method for conducting gene therapy - comprises using recombinant
PT   gene encoding antibody binding antigen associated with a disease;
PT   useful for providing cell immunity.
XX
PS   Example 11; Page 32-33; Table 2; 62pp; English.
XX
CC   A phagemid library was constructed using lymphocyte RNA from
CC   a long-term asymptomatic HIV-1 positive donor.  Heavy and light
CC   chain genes were cloned and a combinatorial library was prepared
CC   and screened to select antigen (HIV rev or tat) binders.  Human
CC   soluble anti-HIV Fabs were obtained.  Heavy chain VH sequences are
CC   given in AAR69084-87, light chain VL in AAR69088-92 and light chain CL
CC   in AAR69093-97.
XX
SQ   Sequence   107 AA;


  Query Match             100.0%;  Score 39;  DB 16;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      47 gknnrps 53


RESULT  13
AAW15528
ID   AAW15528 standard; Protein; 107 AA.
XX
AC   AAW15528;
XX
DT   27-NOV-1997  (first entry)
XX
DE   Anti-TGF beta-2 scFv antibody 14F12 VL domain.
XX
KW   Transforming growth factor beta-2; TGF-beta-2; human;
KW   antibody engineering; scFv; phage display; lung fibrosis;
KW   arterial injury; proliferative retinopathy; retinal detachment;
KW   adult respiratory distress syndrome; liver cirrhosis;
KW   post myocardial infarction; post-angioplasty restenosis;
KW   scleroderma; vascular didease; cataract; glaucoma; scarring;
KW   glomerulonephritis; osteoporosis; immune disease; inflammation;
KW   rheumatoid arthritis; macrophage deficiency disease;
KW   macrophage pathogen infection; therapy; chain shuffling.
XX
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
PN   GB2305921-A.
XX
PD   23-APR-1997.
XX
PF   07-OCT-1996;   96GB-0020920.
XX
PR   19-JAN-1996;   96GB-0001081.
PR   06-OCT-1995;   95GB-0020486.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Bacon L,  Green JA,  Jackson RH,  Johnson KS,  Pope AR;
PI   Tempest PR,  Thompson JE,  Vaughan TJ,  Williams AJ;
PI   Wilton AJ;
XX
DR   WPI; 1997-215360/20.
DR   N-PSDB; AAT60375.
XX
PT   Agent contg. antigen-binding domain of human antibody to
PT   transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT   it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT   immune and inflammatory disease
XX
PS   Claim 5; Fig 2b(v); 184pp; English.
XX
CC   This polypeptide sequence comprises the VL domain of human scFv
CC   antibody 14F12, which is specific for transforming growth factor
CC   (TGF) beta-2.  It is encoded by a gene (AAT60375) isolated from a
CC   light chain shuffle repertoire of a peripheral blood lymphocyte
CC   library.  The antigen-binding domains of human antibodies (see
CC   AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the
CC   adverse effects of TGF beta, such as (i) promotion of fibrosis (in
CC   dermal, ocular or keloid scarring, lung fibrosis, arterial injury,
CC   proliferative retinopathy, retinal detachment, adult respiratory
CC   distress syndrome, liver cirrhosis, post myocardial infarction,
CC   post-angioplasty restenosis, scleroderma, vascular disorders,
CC   cataract, glaucoma, or esp. neural scarring and glomerulonephritis,
CC   also (not claimed) osteoporosis), or (ii) immune and inflammatory
```

```
CC   diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases
CC   or macrophage pathogen infection).  Nucleic acids encoding human
CC   antibody VH and VL can be used for prodn. of recombinant antigen-
CC   binding domains.  These are highly specific, have low dissociation
CC   constants (pref. less than 5 nM) and low IC50s for neutralisation.
XX
SQ   Sequence   107 AA;


  Query Match           100.0%;  Score 39;  DB 18;  Length 107;
  Best Local Similarity  100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     49 gknnrps 55


RESULT  14
AAW08741
ID   AAW08741 standard; Protein; 107 AA.
XX
AC   AAW08741;
XX
DT   08-AUG-1997  (first entry)
XX
DE   Human anti-HIV Fab amino acid sequence tat107(VL4),
XX
KW   Gene therapy; antibody; immunisation; human immunodeficiency virus;
KW   HIV; human T-cell leukaemia virus.
XX
OS   Human Immunodeficiency Virus Type-1.
XX
FH   Key             Location/Qualifiers
FT   Region          1..20
FT                   /label= FR1
FT   Region          21..31
FT                   /label= CDR1
FT   Region          32..46
FT                   /label= FR2
FT   Region          47..58
FT                   /label= CDR2
FT   Region          59..85
FT                   /label= FR3
FT   Region          86..96
FT                   /label= CDR3
FT   Region          97..107
FT                   /label= FR4
FT   Misc-difference 27
FT                   /label= Unspecified
XX
PN   WO9637234-A1.
XX
PD   28-NOV-1996.
XX
PF   23-MAY-1996;   96WO-US07393.
XX
PR   23-MAY-1995;   95US-0447610.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Duan L,  Pomerantz RJ;
XX
DR   WPI; 1997-020948/02.
XX
PT   Improved gene therapy using recombinant gene coding for an antibody
PT   - for intracellular immunisation against pathogens recognised by the
PT   antibody, esp. human immunodeficiency virus HIV-1
XX
PS   Example 11; Page 59-60; 213pp; English.
XX
CC   The present sequence is a human anti-HIV Fab light chain VL sequence.
CC   A novel gene therapy method has been produced, where a recombinant
CC   (rec) gene is introduced into the cells of a mammal. The method is
CC   improved by using a rec gene encoding an antibody (Ab) (e.g. the
CC   present sequence) that is selectively specific for an intracellular
CC   (IC) antigen associated with a disease. The method is used to prevent
CC   or halt the progress of a disease by IC immunisation. Specifically,
CC   the Ab can be used to inhibit the replication of a virus, such as
CC   human T-cell leukaemia virus or especially HIV-1, or of other pathogens,
CC   e.g. bacteria, fungi. The method provides immunity before or after
CC   the development of the disease and can be used to control the
CC   severity of the disease.
XX
SQ   Sequence   107 AA;


  Query Match           100.0%;  Score 39;  DB 18;  Length 107;
  Best Local Similarity  100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     47 gknnrps 53


RESULT  15
AAY95194
ID   AAY95194 standard; Peptide; 107 AA.
XX
AC   AAY95194;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Anti-platelet glycoprotein Ib human HIb-1 VL.
XX
KW   Variable light chain; single chain antibody; scFv; human; HIb-1;
KW   glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW   antithrombotic; thrombus; therapy; diagnostic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..22
FT                   /note= "framework region 1"
FT   Region          23..35
FT                   /note= "complementarity determining region 1"
FT   Region          34..48
FT                   /note= "framework region 2"
FT   Region          49..55
FT                   /note= "complementarity determining region 2"
FT   Region          56..87
FT                   /note= "framework region 3"
FT   Region          88..96
FT                   /note= "complementarity determining region 3"
FT   Region          97..107
FT                   /note= "framework region 4"
XX
PN   WO200026667-A1.
XX
PD   11-MAY-2000.
XX
PF   29-OCT-1999;   99WO-US25495.
XX
PR   30-OCT-1998;   98US-0106275.
XX
PA   (MILL/) MILLER J L.
XX
PI   Miller JL;
XX
DR   WPI; 2000-365744/31.
XX
PT   Isolated nucleic acid molecule encoding anti-human platelet
PT   glycoprotein Ib alpha molecule useful for producing antibodies which
PT   inhibit platelet aggregation -
XX
```

PS Claim 18; Fig 5; 89pp; English.
XX
CC The present sequence is that of the light chain variable region
CC (VL) of human single chain antibody (scFv) HIb-1 (see AAY95198),
CC which is directed against platelet glycoprotein Ib (GPIb). The HIb
CC series of scFv was isolated from a human synthetic VH and VL scFv
CC library by 3 rounds of phagemid selection against transfected CHO
CC cells expressing the GPIb alpha component of the GPIb/IX/V complex
CC on their surface, followed by a 4th round of selection against
CC washed human platelets, and 2 final rounds in which attempts were
CC made to displace scFv from washed platelets by flooding with
CC murine monoclonal antibody or mimotope peptide (see AAY95229).
CC Whether displayed as surface proteins on a phagemid or secreted
CC as free scFv by Escherichia coli, the HIb scFv clones are capable
CC of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPIb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 39; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GKNNRPS 7
           |||||||
Db      49 gknnrps 55
```

Search completed: June 12, 2002, 11:23:34
Job time: 319 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:25:38 ; Search time 61.61 Seconds
(without alignments)
10.917 Million cell updates/sec

Title: US-09-780-035-13
Perfect score: 39
Sequence: 1 GKNNRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

[redacted] number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	96	2	S36060	Ig lambda chain -
2	39	100.0	108	2	S38498	Ig lambda chain -
3	39	100.0	108	2	S47184	Ig lambda chain -
4	39	100.0	109	2	S38496	Ig lambda chain -
5	39	100.0	109	2	S19663	Ig lambda chain V
6	39	100.0	110	2	S36272	Ig lambda chain V
7	39	100.0	115	2	S13726	Ig lambda chain V
8	39	100.0	127	2	S70444	Ig lambda chain pr
9	39	100.0	146	2	S02083	Ig lambda chain V-
10	36	92.3	108	1	L3HUSH	Ig lambda chain V-
11	35	89.7	190	2	S25740	Ig lambda chain -
12	35	89.7	233	2	S25748	Ig lambda chain -
13	34	87.2	233	2	S25741	Ig lambda chain -
14	33	84.6	248	2	H84682	hypothetical prote
15	33	84.6	305	2	A40573	clathrin heavy cha
16	33	84.6	848	2	S59645	probable atp-depen
17	33	84.6	1675	1	LRRTH	clathrin heavy cha
18	32	82.1	110	2	S57442	Ig lambda chain V-
19	32	82.1	1503	2	T18266	cycloinulo-oligosa
20	32	82.1	1858	2	T18273	1-phosphatidylinos
21	31	79.5	406	2	C70851	probable hydrolase
22	31	79.5	432	2	D64046	N-acetylmuramoyl-L
23	31	79.5	585	2	S55205	dihydroxy-acid deh
24	31	79.5	1060	2	S63252	hypothetical prote
25	31	79.5	1181	2	D86157	hypothetical prote
26	31	79.5	1225	2	C84530	hypothetical prote
27	31	79.5	1323	2	E88257	protein let-23 [im
28	31	79.5	1374	2	S70712	protein-tyrosine k
29	30	76.9	58	2	S73144	hypothetical prote
30	30	76.9	93	2	C64684	ribosomal protein
31	30	76.9	93	2	C71835	ribosomal protein
32	30	76.9	110	2	S19672	Ig lambda chain V
33	30	76.9	257	2	G86710	conserved hypothet
34	30	76.9	296	2	T23380	hypothetical prote
35	30	76.9	368	2	G84769	hypothetical prote
36	30	76.9	385	2	I51307	basolateral Na(+)-
37	30	76.9	411	2	S66916	hypothetical prote
38	30	76.9	415	1	JC1494	ribonucleoprotein
39	30	76.9	470	2	T32107	hypothetical prote
40	30	76.9	520	2	AE3563	erythritol kinase
41	30	76.9	526	2	A34896	adenylate cyclase-
42	30	76.9	592	2	T44697	probable ATP-depen
43	30	76.9	658	1	S23391	transcription fact
44	30	76.9	661	2	G97717	hypothetical prote
45	30	76.9	743	2	A87118	ATP-dependent DNA

ALIGNMENTS

RESULT 1
S36060
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36060
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <WIL>
A;Cross-references: EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PID:g312326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 39; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 49 GKNNRPS 55

RESULT 2
S38498
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from
A;Reference number: S38488
A;Accession: S38498
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:Z23035; NID:g414043; PIDN:CAA80570.1; PID:g414044
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 39; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GKNNRPS 7
          |||||||
Db     48 GKNNRPS 54


RESULT   3
S47184
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     49 GKNNRPS 55


RESULT   4
S38496
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38496
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a P
A;Reference number: S38488
A;Accession: S38496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     49 GKNNRPS 55


RESULT   5
S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19663
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276
A;Accession: S19663
A;Molecule type: mRNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     49 GKNNRPS 55


RESULT   6
S36272
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36272
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display librarie
A;Reference number: S36256; MUID:93178448
A;Accession: S36272
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-110 <GRI>
A;Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 0.54;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          |||||||
Db     49 GKNNRPS 55


RESULT   7
S13726
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S13726
R;Frippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 18, 7134, 1990
A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgr
A;Reference number: S13726; MUID:91088295
A;Accession: S13726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <FRI>
A;Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 0.56;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       1 GKNNRPS 7
           |||||||
Db      68 GKNNRPS 74


RESULT   8
S70444
Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70444; S70426
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508
A;Accession: S70444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <CUI>
A;Experimental source: clone E29.1
[redacted]nnelle, C.
[redacted]mitted to the EMBL Data Library, May 1990
A;Reference number: S70426
A;Accession: S70426
A;Molecule type: mRNA
A;Residues: 1-90 <TON>
A;Cross-references: EMBL:X53070
A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F;34-108/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      68 GKNNRPS 74


RESULT   9
S02083
Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N;Alternate names: amyloid-fibril protein GIL
C;Species: Homo sapiens (man)
[redacted]te: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A;Title: The primary structure of the variable region of an immunoglobulin IV light-chai
A;Reference number: S02083; MUID:89134210
A;Accession: S02083
A;Molecule type: protein
A;Residues: 1-70;71-72;73-75;76-131;132-146 <FYK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 39;  DB 2;  Length 146;
  Best Local Similarity   100.0%;  Pred. No. 0.71;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      48 GKNNRPS 54


RESULT  10
L3HUSH
Ig lambda chain V-III region (Sh) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C;Accession: A01980
R;Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The compl
A;Reference number: A92057; MUID:70166723
A;Accession: A01980
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Note: the sequence of the C region is also given
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
F;21-86/Disulfide bonds: #status experimental


  Query Match             92.3%;  Score 36;  DB 1;  Length 108;
  Best Local Similarity   85.7%;  Pred. No. 2.3;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |:|||||
Db      48 GRNNRPS 54


RESULT  11
S25740
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25740
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162
A;Accession: S25740
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-190 <COM>
A;Cross-references: EMBL:X57804; NID:g33705; PIDN:CAA40942.1; PID:g33706
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;105-173/Domain: immunoglobulin homology <IMM>


  Query Match             89.7%;  Score 35;  DB 2;  Length 190;
  Best Local Similarity   85.7%;  Pred. No. 6.4;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |:|||||
Db      25 GQNNRPS 31


RESULT  12
S25748
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162
```

A;Accession: S25748
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|:|||||
Db 68 GENNRPS 74

RESULT 13
S25741
lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25741
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162
A;Accession: S25741
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 34; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
||:||||
Db 68 GKDNRPS 74

RESULT 14
H84682
Hypothetical protein At2g28270 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: H84682
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: H84682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <STO>
A;Cross-references: GB:AE002093; NID:g4803954; PIDN:AAD29826.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g28270
A;Map position: 2
C;Superfamily: Arabidopsis hypothetical protein F4I1.18

Query Match 84.6%; Score 33; DB 2; Length 248;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|| ||||
Db 4 GKTNRPS 10

RESULT 15
A40573
clathrin heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C;Accession: A40573
R;Dodge, G.R.; Kovalszky, I.; McBride, O.W.; Yi, H.F.; Chu, M.; Saitta, B.; Stokes, D
Genomics 11, 174-178, 1991
A;Title: Human clathrin heavy chain (CLTC): partial molecular cloning, expression, an
A;Reference number: A40573; MUID:92112210
A;Accession: A40573
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <DOD>
A;Cross-references: GB:X55878; GB:S75467; NID:g29982; PIDN:CAA39363.1; PID:g29983
C;Superfamily: clathrin heavy chain

Query Match 84.6%; Score 33; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KNNRPS 7
||||||
Db 12 KNNRPS 17

Search completed: June 12, 2002, 11:25:39
Job time: 304 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:39:15 ; Search time 29.47 Seconds
(without alignments)
9.197 Million cell updates/sec

Title: US-09-780-035-13
Perfect score: 39
Sequence: 1 GKNNRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	92.3	108	1	LV3A_HUMAN	P01714 homo sapien
2	33	84.6	848	1	YA47_SCHPO	Q09719 schizosacch
3	33	84.6	1675	1	CLH1_HUMAN	Q00610 homo sapien
4	33	84.6	1675	1	CLH_BOVIN	P49951 bos taurus
5	33	84.6	1675	1	CLH_RAT	P11442 rattus norv
6	32	82.1	1858	1	P3K2_DICDI	P54674 dictyosteli
7	31	79.5	432	1	AMIB_HAEIN	P44493 haemophilus
8	31	79.5	585	1	ILV3_YEAST	P39522 saccharomyc
9	31	79.5	1060	1	YN18_YEAST	P53836 saccharomyc
10	31	79.5	1323	1	LT23_CAEEL	P24348 caenorhabdi
11	30	76.9	58	1	YCX9_PORPU	P51223 porphyra pu
12	30	76.9	75	1	RR16_CYACA	Q9tly9 cyanidium c
13	30	76.9	93	1	RS19_HELPJ	Q9zjr7 helicobacte
14	30	76.9	93	1	RS19_HELPY	P56026 helicobacte
15	30	76.9	395	1	PER_DROEQ	P92203 drosophila
16	30	76.9	396	1	PER_DROPU	P91697 drosophila
17	30	76.9	396	1	PER_DROPV	P91698 drosophila
18	30	76.9	415	1	LA_RAT	P38656 rattus norv
19	30	76.9	526	1	CAP_YEAST	P17555 saccharomyc
20	30	76.9	658	1	TFE2_XENLA	Q01978 xenopus lae
21	30	76.9	743	1	RECG_MYCLE	O69460 mycobacteri
22	30	76.9	1095	1	NKC2_MOUSE	P55014 mus musculu
23	30	76.9	1095	1	NKC2_RAT	P55016 rattus norv
24	30	76.9	1099	1	NKC2_HUMAN	Q13621 homo sapien
25	30	76.9	1099	1	NKC2_RABIT	P55015 oryctolagus
26	30	76.9	1191	1	NKC1_SQUAC	P55013 squalus aca
27	30	76.9	1205	1	NKC1_MOUSE	P55012 mus musculu
28	30	76.9	1212	1	NKC1_HUMAN	P55011 homo sapien
29	30	76.9	1396	1	ITA2_DROME	P12080 drosophila
30	30	76.9	1640	1	CLH2_HUMAN	P53675 homo sapien
31	29	74.4	104	1	YJA7_YEAST	P47080 saccharomyc
32	29	74.4	128	1	Y176_UREPA	Q9pqw7 ureaplasma
33	29	74.4	135	1	VAL2_ICMV	Q08589 indian cass
34	29	74.4	161	1	YJB1_YEAST	P47076 saccharomyc
35	29	74.4	186	1	TLP1_HUMAN	O95753 homo sapien
36	29	74.4	196	1	COAT_BLRV	P19126 bean leafro
37	29	74.4	243	1	YHS7_YEAST	P38833 saccharomyc
38	29	74.4	297	1	XLYA_BACSU	P39800 bacillus su
39	29	74.4	323	1	YCJ5_SCHPO	Q9y7t1 schizosacch
40	29	74.4	348	1	SK1I_RAT	P42572 rattus norv
41	29	74.4	371	1	GAG_FSVST	P03338 feline sarc
42	29	74.4	414	1	GAG_FSVHZ	P04322 feline sarc
43	29	74.4	415	1	LA_MOUSE	P32067 mus musculu
44	29	74.4	416	1	TR16_CHICK	P18519 gallus gall
45	29	74.4	425	1	GAG_FSVGA	P03337 feline sarc

ALIGNMENTS

```
RESULT   1
LV3A_HUMAN
ID   LV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01714;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-III region SH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01980; L3HUSH.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DISULFID     21     86
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11392 MW;  E7E1229586411A56 CRC64;


  Query Match             92.3%;  Score 36;  DB 1;  Length 108;
  Best Local Similarity   85.7%;  Pred. No. 0.67;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
             |:|||||
Db      48 GRNNRPS 54


RESULT   2
YA47_SCHPO
ID   YA47_SCHPO     STANDARD;      PRT;   848 AA.
AC   Q09719;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative ATP-dependent RNA helicase C31A2.07c.
GN   SPAC31A2.07C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE.
CC   -!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. HIGHLY
CC       SIMILAR TO YEAST DBP10.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; Z50113; CAA90465.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR000629; DEAD_ATP_helicase.
DR   InterPro; IPR001650; Helicase_C.
DR   Pfam; PF00270; DEAD; 1.
DR   Pfam; PF00271; helicase_C; 1.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
DR   PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW   Hypothetical protein; ATP-binding; RNA-binding; Helicase.
FT   NP_BIND     113    120       ATP (BY SIMILARITY).
FT   SITE        220    223       DEAD BOX.
SQ   SEQUENCE   848 AA;  94660 MW;  63E9870572BCA074 CRC64;


  Query Match             84.6%;  Score 33;  DB 1;  Length 848;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 KNNRPS 7
           ||||||
Db     839 KNNRPS 844


RESULT   3
CLH1_HUMAN
ID   CLH1_HUMAN     STANDARD;      PRT;  1675 AA.
AC   Q00610;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Clathrin heavy chain 1 (CLH-17).
GN   CLTC OR CLH17 OR KIAA0034.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebratá; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=96051387; PubMed=7584026;
RA   Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,
RA   Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT   "Prediction of the coding sequences of unidentified human genes. I.
RT   The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT   analysis of randomly sampled cDNA clones from human immature myeloid
RT   cell line KG-1.";
RL   DNA Res. 1:27-35(1994).
RN   [2]
RP   SEQUENCE OF 560-864 FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=92112210; PubMed=1765375;
RA   Dodge G.R., Kovalszky I., McBride O.W., Yi H.F., Chu M.L., Saitta B.,
RA   Stokes D.G., Iozzo R.V.;
RT   "Human clathrin heavy chain (CLTC): partial molecular cloning,
RT   expression, and mapping of the gene to human chromosome 17q11-qter.";
RL   Genomics 11:174-178(1991).
CC   -!- FUNCTION: CLATHRIN IS THE MAJOR PROTEIN OF THE POLYHEDRAL COAT OF
CC       COATED PITS & VESICLES. TWO DIFFERENT ADAPTOR PROTEIN COMPLEXES
CC       LINK THE CLATHRIN LATTICE EITHER TO THE PLASMA MEMBRANE OR TO THE
CC       TRANS GOLGI NETWORK.
CC   -!- SUBUNIT: CLATHRIN TRISKELIONS, COMPOSED OF 3 HEAVY CHAINS AND 3
CC       LIGHT CHAINS, ARE THE BASIC SUBUNITS OF THE CLATHRIN COAT. IN THE
CC       PRESENCE OF LIGHT CHAINS, HUB ASSEMBLY IS INFLUENCED BY BOTH THE
CC       PH AND THE CONCENTRATION OF CALCIUM.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC FACE OF COATED PITS AND
CC       VESICLES.
CC   -!- SIMILARITY: BELONGS TO THE CLATHRIN HEAVY CHAIN FAMILY.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; D21260; BAA04801.1; -.
DR   EMBL; X55878; CAA39363.1; -.
DR   PIR; A40573; A40573.
DR   HSSP; P11442; 1BPO.
DR   MIM; 118955; -.
DR   InterPro; IPR001473; Clathrin_propel.
DR   InterPro; IPR000547; Clathrin_repeat.
DR   Pfam; PF01394; Clathrin_propel; 7.
DR   Pfam; PF00637; Clathrin_repeat; 7.
DR   SMART; SM00299; CLH; 7.
KW   Coated pits.
FT   DOMAIN        1    479       GLOBULAR TERMINAL DOMAIN.
FT   DOMAIN      480    523       FLEXIBLE LINKER.
FT   DOMAIN      524   1675       HEAVY CHAIN ARM.
FT   DOMAIN      524    634       DISTAL SEGMENT.
FT   DOMAIN      639   1675       PROXIMAL SEGMENT.
FT   DOMAIN      449    465       BINDING SITE FOR THE UNCOATING ATPASE,
FT                                INVOLVED IN LATTICE DISASSEMBLY
FT                                (POTENTIAL).
FT   BINDING    1213   1522       LIGHT CHAIN (BY SIMILARITY).
FT   DOMAIN     1550   1675       TRIMERIZATION (BY SIMILARITY).
FT   CONFLICT    560    560       Q -> R (IN REF. 2).
FT   CONFLICT    817    817       G -> V (IN REF. 2).
SQ   SEQUENCE   1675 AA;  191614 MW;  6C4F2D54950079E2 CRC64;


  Query Match             84.6%;  Score 33;  DB 1;  Length 1675;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 KNNRPS 7
           ||||||
Db     571 KNNRPS 576


RESULT   4
CLH_BOVIN
ID   CLH_BOVIN      STANDARD;      PRT;  1675 AA.
AC   P49951;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Clathrin heavy chain.
GN   CLTC.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:38:42 ; Search time 107.96 Seconds
(without alignments)
11.217 Million cell updates/sec

Title: US-09-780-035-13
Perfect score: 39
Sequence: 1 GKNNRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	107	4	Q9NSD6	Q9nsd6 homo sapien
2	33	84.6	248	10	Q9SL28	Q9sl28 arabidopsis
3	33	84.6	515	10	Q9LUD2	Q9lud2 arabidopsis
4	33	84.6	531	3	O94748	O94748 neurospora
5	32	82.1	626	3	O42790	O42790 neurospora
6	32	82.1	626	3	O42791	O42791 neurospora
7	32	82.1	1333	2	Q9F0I5	Q9f0i5 paenibacill
8	32	82.1	1503	2	O52973	O52973 bacillus ci
9	31	79.5	272	12	Q997I9	Q997i9 bovine aden
10	31	79.5	406	2	Q93AQ2	Q93aq2 mycobacteri
11	31	79.5	406	16	O53593	O53593 mycobacteri
12	31	79.5	699	2	Q51287	Q51287 neisseria m
13	31	79.5	1181	10	Q9SRW9	Q9srw9 arabidopsis
14	31	79.5	1225	10	Q9ZQF8	Q9zqf8 arabidopsis
15	31	79.5	1260	5	Q9W2Y5	Q9w2y5 drosophila
16	31	79.5	1484	4	Q9BXF3	Q9bxf3 homo sapien
17	30	76.9	212	9	Q9MBS2	Q9mbs2 staphylococ
18	30	76.9	257	16	Q9CHP1	Q9chp1 lactococcus
19	30	76.9	296	5	O01340	O01340 caenorhabdi
20	30	76.9	297	12	Q9III1	Q9iii1 frog adenov
21	30	76.9	319	10	Q9LHS3	Q9lhs3 arabidopsis
22	30	76.9	368	10	O82288	O82288 arabidopsis
23	30	76.9	379	17	Q97AS9	Q97as9 thermoplasm
24	30	76.9	385	13	Q91412	Q91412 necturus ma
25	30	76.9	411	3	Q08412	Q08412 saccharomyc
26	30	76.9	417	5	Q9V4V1	Q9v4v1 drosophila
27	30	76.9	421	5	Q9BIC9	Q9bic9 trichinella
28	30	76.9	425	6	Q28759	Q28759 procavia ca
29	30	76.9	455	3	O94232	O94232 kluyveromyc
30	30	76.9	470	5	O16747	O16747 caenorhabdi
31	30	76.9	519	2	Q9ZB32	Q9zb32 brucella ab
32	30	76.9	538	2	Q9S4A4	Q9s4a4 actinobacil
33	30	76.9	574	4	Q9UJG6	Q9ujg6 homo sapien
34	30	76.9	574	4	Q9Y2Z5	Q9y2z5 homo sapien
35	30	76.9	578	4	Q969N2	Q969n2 homo sapien
36	30	76.9	578	11	Q99JA3	Q99ja3 mus musculu
37	30	76.9	601	10	Q94AV3	Q94av3 arabidopsis
38	30	76.9	656	17	Q97AI4	Q97ai4 thermoplasm
39	30	76.9	661	16	Q92JC4	Q92jc4 rickettsia
40	30	76.9	688	5	Q9VBE6	Q9vbe6 drosophila
41	30	76.9	711	2	Q9ZFD4	Q9zfd4 moraxella c
42	30	76.9	712	2	Q9ZI06	Q9zi06 moraxella c
43	30	76.9	713	2	O85051	O85051 moraxella c
44	30	76.9	759	10	Q9SIX2	Q9six2 arabidopsis
45	30	76.9	770	11	Q9Z1E0	Q9z1e0 mus musculu

ALIGNMENTS

RESULT 1
Q9NSD6
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOCYTE;
RA Hohmann A.;
RT "Autoimmunity.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L43092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 100.0%; Score 39; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 47 GKNNRPS 53

RESULT 2

```
Q9SL28
ID   Q9SL28      PRELIMINARY;      PRT;   248 AA.
AC   Q9SL28;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AT2G28270 PROTEIN.
GN   AT2G28270.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC006202; AAD29826.1; -.
DR   InterPro; IPR004146; DC1.
DR   InterPro; IPR001965; PHD.
DR   Pfam; PF03107; DC1; 2.
DR   SMART; SM00249; PHD; 1.
SQ   SEQUENCE   248 AA;  28016 MW;  4A2D79F034C209DB CRC64;


  Query Match             84.6%;  Score 33;  DB 10;  Length 248;
  Best Local Similarity   85.7%;  Pred. No. 35;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           || ||||
Db       4 GKTNRPS 10


ULT   3
Q9LUD2
ID   Q9LUD2      PRELIMINARY;      PRT;   515 AA.
AC   Q9LUD2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYTOCHROME P450 (AT3G14620/MIE1_12).
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA   Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA   Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA   Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA   Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA   Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA   Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AB023038; BAB02394.1; -.
DR   EMBL; AY052208; AAK97679.1; -.
DR   InterPro; IPR001128; Cyt_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   515 AA;  58643 MW;  9F4EFCF7686F55A1 CRC64;


  Query Match             84.6%;  Score 33;  DB 10;  Length 515;
  Best Local Similarity   71.4%;  Pred. No. 73;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
             ||||:|:
Db     358 GKNNKPN 364


RESULT   4
O94748
ID   O94748      PRELIMINARY;      PRT;   531 AA.
AC   O94748;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   PROTEIN PHOSPHATASE-Z-LIKE SERINE/THREONINE PROTEIN PHOSPHATASE.
GN   PZL-1.
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98449783; PubMed=9774742;
RA   Szoor B., Feher Z., Zeke T., Gergely P., Yatzkan E., Yarden O.,
RA   Dombradi V.;
RT   "pzl-1 encodes a novel protein phosphatase-Z-like Ser/Thr protein
RT   phosphatase in Neurospora crassa.";
RL   Biochim. Biophys. Acta 1388:260-266(1998).
CC   -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC       ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC   -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR   EMBL; AF071752; AAD09996.1; -.
DR   EMBL; AF071751; AAD09995.1; -.
DR   HSSP; P08129; 1FJM.
DR   InterPro; IPR000934; Ser_thr_phosphtse.
DR   Pfam; PF00149; STphosphatase; 1.
DR   PRINTS; PR00114; STPHPHTASE.
DR   SMART; SM00156; PP2Ac; 1.
DR   PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW   Hydrolase; Iron; Manganese.
SQ   SEQUENCE   531 AA;  58311 MW;  D9D3B71EA704F736 CRC64;


  Query Match             84.6%;  Score 33;  DB 3;  Length 531;
  Best Local Similarity   85.7%;  Pred. No. 76;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:29 ; Search time 49.09 Seconds
(without alignments)
3.483 Million cell updates/sec

Title: US-09-780-035-13
Perfect score: 39
Sequence: 1 GKNNRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	67	2	US-08-273-146-67	Sequence 67, Appl
2	39	100.0	97	2	US-08-665-202-35	Sequence 35, Appl
3	39	100.0	103	2	US-08-273-146-71	Sequence 71, Appl
4	39	100.0	104	4	US-08-793-450-2	Sequence 2, Appli
5	39	100.0	109	2	US-08-652-816A-16	Sequence 16, Appl
6	39	100.0	109	2	US-08-665-202-34	Sequence 34, Appl
7	39	100.0	238	4	US-08-793-450-6	Sequence 6, Appli
8	39	100.0	278	4	US-09-260-527-3	Sequence 3, Appli
9	39	100.0	280	4	US-09-260-527-1	Sequence 1, Appli
10	39	100.0	309	4	US-09-079-029-9	Sequence 9, Appli
11	39	100.0	312	4	US-09-079-029-10	Sequence 10, Appl
12	36	92.3	106	4	US-09-240-274-47	Sequence 47, Appl
13	36	92.3	106	4	US-09-240-274-48	Sequence 48, Appl
14	34	87.2	104	4	US-09-240-274-49	Sequence 49, Appl
15	33	84.6	131	1	US-08-305-683A-4	Sequence 4, Appli
16	32	82.1	2123	4	US-08-968-685A-10	Sequence 10, Appl
17	31	79.5	580	4	US-09-188-930-307	Sequence 307, App
18	30	76.9	707	2	US-08-949-941B-2	Sequence 2, Appli
19	30	76.9	1070	3	US-08-613-009A-11	Sequence 11, Appl
20	30	76.9	1212	4	US-09-268-866-2	Sequence 2, Appli
21	29	74.4	7	4	US-08-918-148-10	Sequence 10, Appl
22	29	74.4	110	4	US-09-240-274-65	Sequence 65, Appl
23	29	74.4	112	4	US-09-240-274-64	Sequence 64, Appl
24	29	74.4	186	3	US-08-705-771-14	Sequence 14, Appl
25	29	74.4	249	4	US-08-918-148-74	Sequence 74, Appl
26	29	74.4	348	1	US-08-035-392-2	Sequence 2, Appli
27	29	74.4	348	1	US-08-504-511A-2	Sequence 2, Appli
28	29	74.4	430	1	US-08-035-392-4	Sequence 4, Appli
29	29	74.4	430	1	US-08-504-511A-4	Sequence 4, Appli
30	29	74.4	1545	4	US-08-296-791-4	Sequence 4, Appli
31	29	74.4	1545	5	PCT-US95-10661A-4	Sequence 4, Appli
32	28.5	73.1	3289	2	US-08-477-451-2	Sequence 2, Appli
33	28	71.8	12	4	US-08-672-850-18	Sequence 18, Appl
34	28	71.8	106	1	US-08-488-113B-152	Sequence 152, App
35	28	71.8	106	1	US-08-477-484B-152	Sequence 152, App
36	28	71.8	106	1	US-08-107-669D-16	Sequence 16, Appl
37	28	71.8	106	1	US-08-472-788A-16	Sequence 16, Appl
38	28	71.8	106	2	US-08-477-531B-16	Sequence 16, Appl
39	28	71.8	106	2	US-08-646-360-152	Sequence 152, App
40	28	71.8	106	2	US-08-082-842A-16	Sequence 16, Appl
41	28	71.8	106	4	US-08-839-765-152	Sequence 152, App
42	28	71.8	106	4	US-09-136-389-152	Sequence 152, App
43	28	71.8	110	4	US-09-240-274-63	Sequence 63, Appl
44	28	71.8	132	2	US-08-345-321-4	Sequence 4, Appli
45	28	71.8	236	4	US-09-049-672A-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT   1
US-08-273-146-67
; Sequence 67, Application US/08273146
; Patent No. 5855885
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Rodger
;    APPLICANT:  McCafferty, John
;    APPLICANT:  Chiswell, David
;    APPLICANT:  Darsley, Michael J.
;    APPLICANT:  Fitzgerald, Kevin
;    APPLICANT:  Kenten, John H.
;    APPLICANT:  Martin, Mark T.
;    APPLICANT:  Titmas, Richard C.
;    APPLICANT:  Williams, Richard O.
;    TITLE OF INVENTION:  The Isolation and Production of
;    TITLE OF INVENTION:  Catalytic Antibodies using Phage Technology
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IGEN, Inc.
;      STREET:  1530 East Jefferson St.
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20852
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,146
;      FILING DATE:  14-JUL-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ryan, John W.
;      REGISTRATION NUMBER:  33,771
;      REFERENCE/DOCKET NUMBER:  09000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-984-8000
;      TELEFAX:  301-230-0158
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  67 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-273-146-67


  Query Match                 100.0%;  Score 39;  DB 2;  Length 67;
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  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db       6 GKNNRPS 12


RESULT   2
US-08-665-202-35
; Sequence 35, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  97 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-35


  Query Match             100.0%;  Score 39;  DB 2;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      48 GKNNRPS 54


RESULT   3
US-08-273-146-71
; Sequence 71, Application US/08273146
; Patent No. 5855885
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Rodger
;    APPLICANT:  McCafferty, John
;    APPLICANT:  Chiswell, David
;    APPLICANT:  Darsley, Michael J.
;    APPLICANT:  Fitzgerald, Kevin
;    APPLICANT:  Kenten, John H.
;    APPLICANT:  Martin, Mark T.
;    APPLICANT:  Titmas, Richard C.
;    APPLICANT:  Williams, Richard O.
;    TITLE OF INVENTION:  The Isolation and Production of
;    TITLE OF INVENTION:  Catalytic Antibodies using Phage Technology
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IGEN, Inc.
;      STREET:  1530 East Jefferson St.
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20852
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,146
;      FILING DATE:  14-JUL-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ryan, John W.
;      REGISTRATION NUMBER:  33,771
;      REFERENCE/DOCKET NUMBER:  09000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-984-8000
;      TELEFAX:  301-230-0158
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  103 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-273-146-71


  Query Match             100.0%;  Score 39;  DB 2;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 0.65;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      43 GKNNRPS 49


RESULT   4
US-08-793-450-2
; Sequence 2, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT:  EDELMAN, LENA
;    APPLICANT:  MARGARITTE, CHRISTEL
;    APPLICANT:  KACZOREK, MICHEL
;    APPLICANT:  CHAABIHI, HASSAN
;    TITLE OF INVENTION:  MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,450
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10566
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-450-2


  Query Match             100.0%;  Score 39;  DB 4;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 0.65;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      49 GKNNRPS 55


RESULT   5
US-08-652-816A-16
; Sequence 16, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-16


  Query Match             100.0%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      49 GKNNRPS 55


RESULT   6
US-08-665-202-34
; Sequence 34, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
```

```
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-34


  Query Match           100.0%;  Score 39;  DB 2;  Length 109;
  Best Local Similarity  100.0%;  Pred. No. 0.68;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      48 GKNNRPS 54


RESULT   7
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
;  GENERAL INFORMATION:
;    APPLICANT:  EDELMAN, LENA
;    APPLICANT:  MARGARITTE, CHRISTEL
;    APPLICANT:  KACZOREK, MICHEL
;    APPLICANT:  CHAABIHI, HASSAN
;    TITLE OF INVENTION:  MONOCLONAL RECOMBINANT ANTI-RHESUS D
;    TITLE OF INVENTION:
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,450
;      FILING DATE:  03-MAR-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/10566
;      FILING DATE:  02-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-450-6


  Query Match           100.0%;  Score 39;  DB 4;  Length 238;
  Best Local Similarity  100.0%;  Pred. No. 1.5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db      68 GKNNRPS 74


RESULT   8
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
;  APPLICANT: Knox, J.P.
;  APPLICANT: Mikkelsen, J.D.
;  APPLICANT: Willats, W. G.
;  TITLE OF INVENTION: ANTIBODY
;  FILE REFERENCE: DYOU19.001AUS
;  CURRENT APPLICATION NUMBER: US/09/260,527A
;  CURRENT FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 278
;   TYPE: PRT
;   ORGANISM: UNKNOWN
;   FEATURE:
;   OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
;   OTHER INFORMATION: from a naive phage display library known as the
;   OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
;   OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3


  Query Match           100.0%;  Score 39;  DB 4;  Length 278;
  Best Local Similarity  100.0%;  Pred. No. 1.7;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db     201 GKNNRPS 207


RESULT   9
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
;  APPLICANT: Knox, J.P.
;  APPLICANT: Mikkelsen, J.D.
;  APPLICANT: Willats, W. G.
;  TITLE OF INVENTION: ANTIBODY
;  FILE REFERENCE: DYOU19.001AUS
;  CURRENT APPLICATION NUMBER: US/09/260,527A
;  CURRENT FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: UNKNOWN
;   FEATURE:
;   OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
;   OTHER INFORMATION: phage display library known as the Synthetic scFv
;   OTHER INFORMATION: Library (#1) from the Centre for Protein
;   OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1


  Query Match           100.0%;  Score 39;  DB 4;  Length 280;
  Best Local Similarity  100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db     203 GKNNRPS 209
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```
RESULT  10
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;     APPLICANT:  Adams, Camilia W.
;     APPLICANT:  Ashkenazi, Avi J.
;     APPLICANT:  Chuntharapai, Anan
;     APPLICANT:  Kim, Kyung J.
;     TITLE OF INVENTION:  Apo-2 Receptor
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  1 DNA Way
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/079,029
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marschang, Diane L.
;       REGISTRATION NUMBER:  35,600
;       REFERENCE/DOCKET NUMBER:  P1101R2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-5416
;       TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  309 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-09-079-029-9


  Query Match             100.0%;  Score 39;  DB 4;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db     223 GKNNRPS 229


RESULT  11
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;     APPLICANT:  Adams, Camilia W.
;     APPLICANT:  Ashkenazi, Avi J.
;     APPLICANT:  Chuntharapai, Anan
;     APPLICANT:  Kim, Kyung J.
;     TITLE OF INVENTION:  Apo-2 Receptor
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  1 DNA Way
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/079,029
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marschang, Diane L.
;       REGISTRATION NUMBER:  35,600
;       REFERENCE/DOCKET NUMBER:  P1101R2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-5416
;       TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  312 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-09-079-029-10


  Query Match             100.0%;  Score 39;  DB 4;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||||||
Db     226 GKNNRPS 232


RESULT  12
US-09-240-274-47
; Sequence 47, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J01
US-09-240-274-47


  Query Match             92.3%;  Score 36;  DB 4;  Length 106;
  Best Local Similarity   85.7%;  Pred. No. 2.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |:||||
Db      47 GRNNRPS 53


RESULT  13
US-09-240-274-48
; Sequence 48, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
```

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;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J02
US-09-240-274-48


  Query Match           92.3%;  Score 36;  DB 4;  Length 106;
  Best Local Similarity  85.7%;  Pred. No. 2.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |:|||||
Db      47 GRNNRPS 53


RESULT  14
US-09-240-274-49
; Sequence 49, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49


  Query Match           87.2%;  Score 34;  DB 4;  Length 104;
  Best Local Similarity  85.7%;  Pred. No. 6.3;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           |||:|||
Db      47 GKNSRPS 53


RESULT  15
US-08-305-683A-4
; Sequence 4, Application US/08305683A
; Patent No. 5646041
;  GENERAL INFORMATION:
;    APPLICANT:  HARFELDT, Elisabeth
;    APPLICANT:  LAKE, Philip
;    APPLICANT:  NOTTAGE, Barbara
;    APPLICANT:  OSTBERG, Lars G.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY TO HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS AND CELL LINE PRODUCING THE SAME
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/305,683A
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/759,279
;      FILING DATE:  13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  11823-005230
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  131 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-305-683A-4


  Query Match           84.6%;  Score 33;  DB 1;  Length 131;
  Best Local Similarity  85.7%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GKNNRPS 7
           | |||||
Db      71 GDNNRPS 77


Search completed: June 12, 2002, 11:24:30
Job time: 265 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:23:34 ; Search time 136.11 Seconds
(without alignments)
8.977 Million cell updates/sec

Title: US-09-780-035-14
Perfect score: 55
Sequence: 1 GSRDSSGIHVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	11	22	AAG65304	Anti-IL-18 antibod
2	55	100.0	109	22	AAG65309	Anti-IL-18 antibod
3	55	100.0	109	22	AAG65353	Anti-IL-18 antibod
4	42	76.4	11	22	AAG62970	Complementarity de
5	42	76.4	11	22	AAG62974	Complementarity de
6	42	76.4	11	22	AAG62976	Complementarity de
7	42	76.4	11	22	AAG62980	Complementarity de
8	42	76.4	11	22	AAG62984	Complementarity de
9	42	76.4	101	13	AAR22572	Light chain VL3.5
10	42	76.4	107	22	AAG62943	Amino acid sequenc
11	42	76.4	107	22	AAG62969	Amino acid sequenc
12	42	76.4	108	21	AAY44616	Human antibody clo
13	42	76.4	108	22	AAG62933	Amino acid sequenc
14	42	76.4	108	22	AAG62937	Amino acid sequenc
15	42	76.4	108	22	AAG62939	Amino acid sequenc
16	42	76.4	109	18	AAW19884	CEA-specific antib
17	42	76.4	109	18	AAW15525	Anti-TGF beta-2 sc
18	42	76.4	109	22	AAU02504	Anti-adipocyte mon
19	42	76.4	109	22	AAU02509	Anti-adipocyte mon
20	42	76.4	109	22	AAU02513	Anti-adipocyte mon
21	42	76.4	112	22	AAG62947	Amino acid sequenc
22	42	76.4	229	19	AAW49694	Human ScFv5 agains
23	42	76.4	236	19	AAW49690	Human ScFv1 agains
24	42	76.4	237	19	AAW49691	Human ScFv2 agains
25	42	76.4	239	19	AAW49692	Human ScFv3 agains
26	42	76.4	249	18	AAW24061	Human WSX receptor
27	42	76.4	254	19	AAW49693	Human ScFv4 agains
28	42	76.4	280	22	AAE02186	PAM2 single chain
29	42	76.4	282	22	AAE02185	PAM1 single chain
30	42	76.4	309	20	AAW83322	Single chain Apo-2
31	42	76.4	312	20	AAW83323	Single chain Apo-2
32	41	74.5	309	21	AAG22955	Arabidopsis thalia
33	41	74.5	389	21	AAG22954	Arabidopsis thalia
34	41	74.5	453	21	AAG22953	Arabidopsis thalia
35	39	70.9	11	22	AAG62972	Complementarity de
36	39	70.9	11	22	AAG62982	Complementarity de
37	39	70.9	11	22	AAG62998	Complementarity de
38	39	70.9	106	22	AAU02518	Anti-adipocyte mon
39	39	70.9	106	22	AAU02531	Anti-adipocyte mon
40	39	70.9	108	22	AAG62935	Amino acid sequenc
41	39	70.9	108	22	AAG62945	Amino acid sequenc
42	39	70.9	108	22	AAG62961	Amino acid sequenc
43	39	70.9	109	18	AAW15559	TGF beta-1/TGF bet
44	39	70.9	109	22	AAU02527	Anti-adipocyte mon
45	39	70.9	115	22	AAG65559	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAG65304
ID AAG65304 standard; protein; 11 AA.
XX
AC AAG65304;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR3 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 27; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain CDR3 fragment.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 55; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSRDSSGIHVV 11
||||||||||||
Db 1 gsrdssgihvv 11

RESULT 2
AAG65309
ID AAG65309 standard; protein; 109 AA.
XX
AC AAG65309;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47512.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 55; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSRDSSGIHVV 11
||||||||||||
Db 88 gsrdssgihvv 98

RESULT 3
AAG65353
ID AAG65353 standard; protein; 109 AA.
XX
AC AAG65353;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain sequence.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
DR N-PSDB; AAH47512.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Example 2; Page 88; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 55; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSRDSSGIHVV 11
||||||||||| |
Db 88 gsrdssgihvv 98

RESULT 4
AAG62970
ID AAG62970 standard; peptide; 11 AA.
XX
AC AAG62970;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G65.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 5
AAG62974
ID AAG62974 standard; peptide; 11 AA.
XX
AC AAG62974;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G73.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving

CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 6
AAG62976
ID AAG62976 standard; peptide; 11 AA.
XX
AC AAG62976;
XX
01-OCT-2001 (first entry)
DE Complementarity determining region 3 (CDR3) of VL chain of clone G76.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 7
AAG62980
ID AAG62980 standard; peptide; 11 AA.
XX
AC AAG62980;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G78.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

```
RESULT   8
AAG62984
ID   AAG62984 standard; peptide; 11 AA.
XX
AC   AAG62984;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Complementarity determining region 3 (CDR3) of VL chain of clone G81.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases -
XX
PS   Claim 1; Page 76; 109pp; English.
XX
CC   AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC   of VL and VH chains of antibodies of the invention. The specification
CC   describes a mixture or panel of 5 different specific binding members,
CC   each comprising an antibody VH and/or VL variable domain and capable,
CC   when displayed on the surface of filamentous bacteriophage particles or
CC   in the case of a specific binding member comprising the D5 VH and/or VL
CC   variable domain when bound to human serum amyloid protein, to pass
CC   through a mammalian blood brain barrier (BBB). The panel is useful for
CC   the selection of specific binding members with a desired property such
CC   as ability to cross BBB, ability to bind endothelial cells or other brain
CC   cell antigen, ability to bind areas of inflammation in the brain or BBB
CC   breakdown or ability to bind intracellular adhesion molecules and to bind
CC   transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC   and treatment of human or animal body, including neurological diseases,
CC   such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC   epilepsy and traumatic brain injury and any diseases involving
CC   inflammation occurring within the brain or central nervous system.
XX
SQ   Sequence   11 AA;


  Query Match             76.4%;  Score 42;  DB 22;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 0.097;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| ||| 
Db       2 srdssgnhvv 11


RESULT   9
AAR22572
ID   AAR22572 standard; Protein; 101 AA.
XX
AC   AAR22572;
XX
DT   21-MAY-1992  (first entry)
XX
DE   Light chain VL3.5 from BSA binding scFv fragment.
XX
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; human.
XX
OS   Homo sapiens.
XX
PN   WO9201047-A.
XX
PD   23-JAN-1992.
XX
PF   10-JUL-1991;   91WO-GB01134.
XX
PR   15-MAY-1991;   91GB-0010549.
PR   10-JUL-1990;   90GB-0015198.
PR   19-OCT-1990;   90GB-0022845.
PR   12-NOV-1990;   90GB-0024503.
PR   06-MAR-1991;   91GB-0004744.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
XX
PI   McCafferty J,  Pope AR,  Johnson KS,  Hoogenboom HRJ,  Griffiths AD;
PI   Jackson RH,  Holliger KP,  Marks JD,  Clackson TP,  Chiswell DJ;
PI   Winter GP,  Bonnert TP;
XX
DR   WPI; 1992-056862/07.
XX
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
XX
PS   Table 11; Page 152; 109pp; English.
XX
CC   PCR was used to prepare a human scFv library from RNA from white
CC   blood cells from an unimmunised donor.  Heavy chains from IgG and
CC   IgM antibodies were amplified separately.  Four separate libraries
CC   were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
CC   purified scFv fragments were ligated into the phagemid pHEN1 for
CC   expression on the surface of fd bacteriophage as gene III fusions.
CC   The clones were then subjected to affinity selection for binding
CC   to phOx:BSA by selection on tubes followed by analysis by ELISA. Of
CC   96 clones analysed, 43 showed binding to both phOx:BSA and BSA.
CC   These were designated BSA binders.  Thirteen of fourteen clones
CC   sequenced had the same sequence, the VH derived from a human VH3
CC   family gene (AAR22571) and the VL from a human V lambda 3 family
CC   gene (shown here).  The other was derived from a human VH4 family
CC   gene and a human Vk1 family gene. One clone bound only to phOx:BSA
CC   (oxazolone binder).  This sequence revealed a VH derived from a
CC   human VH1 family gene (AAR22569) and VL from a human V lambda 1
CC   family gene (AAR22570).
CC   See also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
XX
SQ   Sequence   101 AA;


  Query Match             76.4%;  Score 42;  DB 13;  Length 101;
  Best Local Similarity   90.0%;  Pred. No. 1.3;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| ||| 
Db      89 srdssgnhvv 98


RESULT  10
AAG62943
ID   AAG62943 standard; Protein; 107 AA.
```

XX
AC AAG62943;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone G78.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
[redacted] 13-DEC-1999; 99US-0170599.
XX
[redacted] (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42387.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 96; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
[redacted] treatment of human or animal body, including neurological diseases, such
[redacted] as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
[redacted] and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 107 AA;

Query Match 76.4%; Score 42; DB 22; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 87 srdssgnhvv 96

RESULT 11
AAG62969
ID AAG62969 standard; Protein; 107 AA.
XX
AC AAG62969;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone D5.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42412.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 109; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 107 AA;

Query Match 76.4%; Score 42; DB 22; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 87 srdssgnhvv 96

RESULT 12
AAY44616
ID AAY44616 standard; Protein; 108 AA.
XX
AC AAY44616;
XX
DT 07-APR-2000 (first entry)
XX
DE Human antibody clone NHS76 VL.
XX
KW Human antibody clone NHS76 VL; VL; light chain variable region;
KW cytostatic; malignant tumour; human histone H1; antibody;
KW intracellular antigen; diagnosis; treatment; tumour; cervical; ovarian;

```
KW   prostate; lung; liver; pancreatic; colon; stomach; prodrug.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          23..33
FT                   /label= Complementarity_determining_region_1
FT   Domain          49..55
FT                   /label= Complementarity_determining_region_2
FT   Domain          88..98
FT                   /label= Complementarity_determining_region_3
XX
PN   WO200001822-A1.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-GB02123.
XX
PR   02-JUL-1998;   98GB-0014383.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Williams AJ,  Tempest PR,  Holtet TL,  Jackson H;
XX
DR   WPI; 2000-137204/12.
DR   N-PSDB; AAZ49591.
XX
PT   New specific binding members capable of binding an intracellular
PT   antigen, useful in the treatment and diagnosis of tumours -
XX
PS   Claim 5; Fig 2; 70pp; English.
XX
CC   The present sequence is human antibody clone NHS76 light chain
CC   variable region. This is useful for targeting the necrotic centres of
CC   malignant tumours by binding to human histone H1 and other intracellular
CC   antigens. The specific binding members based on the CDRs
CC   (complementarity determining regions) of NHS76 can be used in diagnosis
CC   and treatment of tumours like cervical, ovarian, prostate, lung, liver,
CC   pancreatic, colon and stomach tumours. The antibody is labelled with
CC   functional labels such as toxins and enzymes which are capable of
CC   converting prodrugs into active drugs at the site of a tumour.
XX
SQ   Sequence   108 AA;


  Query Match             76.4%;  Score 42;  DB 21;  Length 108;
  Best Local Similarity   90.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| |||
Db      89 srdssgnhvv 98


RESULT  13
AAG62933
ID   AAG62933 standard; Protein; 108 AA.
XX
AC   AAG62933;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Amino acid sequence of variable light chain fragment of clone G65.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
DR   N-PSDB; AAH42377.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases -
XX
PS   Claim 1; Page 91; 109pp; English.
XX
CC   The present sequence represents an antibody variable light chain (VL)
CC   fragment. The fragment is used to produce a mixture or panel of 5
CC   different specific binding members, each comprising an antibody VH
CC   and/or VL variable domain and capable, when displayed on the surface
CC   of filamentous bacteriophage particles or in the case of a specific
CC   binding member comprising the D5 VH and/or VL variable domain when
CC   bound to human serum amyloid protein, to pass through a mammalian
CC   blood brain barrier (BBB). The panel is useful for the selection of
CC   specific binding members with a desired property such as ability to
CC   cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC   ability to bind areas of inflammation in the brain or BBB breakdown or
CC   ability to bind intracellular adhesion molecules and to bind transferrin
CC   receptor. The antibodies are useful in diagnosis, prophylaxis and
CC   treatment of human or animal body, including neurological diseases, such
CC   as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC   and traumatic brain injury and any diseases involving inflammation
CC   occurring within the brain or central nervous system.
XX
SQ   Sequence   108 AA;


  Query Match             76.4%;  Score 42;  DB 22;  Length 108;
  Best Local Similarity   90.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| |||
Db      88 srdssgnhvv 97


RESULT  14
AAG62937
ID   AAG62937 standard; Protein; 108 AA.
XX
AC   AAG62937;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Amino acid sequence of variable light chain fragment of clone G73.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
```

XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42381.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 93; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 108 AA;

Query Match 76.4%; Score 42; DB 22; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 88 srdssgnhvv 97

RESULT 15
AAG62939
ID AAG62939 standard; Protein; 108 AA.
XX
AC AAG62939;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of variable light chain fragment of clone G76.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
DR N-PSDB; AAH42383.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 94; 109pp; English.
XX
CC The present sequence represents an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH
CC and/or VL variable domain and capable, when displayed on the surface
CC of filamentous bacteriophage particles or in the case of a specific
CC binding member comprising the D5 VH and/or VL variable domain when
CC bound to human serum amyloid protein, to pass through a mammalian
CC blood brain barrier (BBB). The panel is useful for the selection of
CC specific binding members with a desired property such as ability to
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,
CC ability to bind areas of inflammation in the brain or BBB breakdown or
CC ability to bind intracellular adhesion molecules and to bind transferrin
CC receptor. The antibodies are useful in diagnosis, prophylaxis and
CC treatment of human or animal body, including neurological diseases, such
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
CC and traumatic brain injury and any diseases involving inflammation
CC occurring within the brain or central nervous system.
XX
SQ Sequence 108 AA;

Query Match 76.4%; Score 42; DB 22; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 88 srdssgnhvv 97

Search completed: June 12, 2002, 11:23:34
Job time: 319 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:25:39 ; Search time 61.61 Seconds
(without alignments)
17.156 Million cell updates/sec

Title: US-09-780-035-14
Perfect score: 55
Sequence: 1 GSRDSSGIHVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	76.4	108	2	S47184	Ig lambda chain -
2	42	76.4	109	2	S19663	Ig lambda chain V
3	41	74.5	389	2	B96635	hypothetical prote
4	39	70.9	108	1	L3HUSH	Ig lambda chain V-
5	39	70.9	190	2	S25740	Ig lambda chain -
6	39	70.9	622	2	T49426	Type 2C Protein Ph
7	38	69.1	450	2	C89771	Immunoglobulin G b
8	38	69.1	508	2	A29605	protein A precurso
9	38	69.1	524	1	QVSAA	protein A precurso
10	37	67.3	127	2	S70444	Ig lambda chain pr
11	37	67.3	374	2	F86243	ZIP4, probable zin
12	37	67.3	979	2	B57282	ankyrin-related pr
13	37	67.3	1786	2	A57282	ankyrin-related pr
14	37	67.3	1815	2	T15346	elegans ankyrin-re
15	37	67.3	1867	2	T15344	ankyrin-related un
16	37	67.3	2039	2	T15347	ankyrin-related un
17	36.5	66.4	287	2	D75177	dolichyl-phosphate
18	36	65.5	109	2	S38496	Ig lambda chain -
19	36	65.5	109	2	D71528	probable pts phosp
20	36	65.5	552	2	A46564	thermolysin (EC 3.
21	35	63.6	149	2	B72735	hypothetical prote
22	35	63.6	176	2	T29845	hypothetical prote
23	35	63.6	243	2	E48326	cytb intron 3a pro
24	35	63.6	281	2	B71552	probable sua5-rela
25	35	63.6	429	1	T03607	probable carboxype
26	35	63.6	481	2	T21550	hypothetical prote
27	35	63.6	527	2	PN0114	microbial metallop
28	35	63.6	548	1	HYBST	thermolysin (EC 3.
29	35	63.6	551	2	B36706	neutral proteinase
30	35	63.6	573	2	T25397	hypothetical prote
31	35	63.6	576	2	A71497	probable DNA misma
32	35	63.6	610	2	A33650	dopamine beta-mono
33	35	63.6	619	2	S45932	tyrosine transport
34	35	63.6	620	2	A61086	dopamine beta-mono
35	35	63.6	633	2	D64222	DNA topoisomerase
36	35	63.6	648	1	P3BPF6	P3 protein - phage
37	35	63.6	1377	2	T51447	transcription regu
38	35	63.6	7962	2	I38346	elastic titin - hu
39	34	61.8	96	2	S36060	Ig lambda chain -
40	34	61.8	115	2	S13726	Ig lambda chain V
41	34	61.8	263	2	C65098	exu regulon regula
42	34	61.8	263	2	H91125	negative regulator
43	34	61.8	263	2	G85970	exu regulon regula
44	34	61.8	273	2	H69206	dihydrodipicolinat
45	34	61.8	298	2	T50448	3-mercaptopyruvate

ALIGNMENTS

RESULT 1
S47184
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from pat
A;Reference number: S47181
A;Accession: S47184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 SRDSSGIHVV 11
           |||||| |||
Db      89 SRDSSGNHVV 98
```

RESULT 2
S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19663
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Wint
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on
A;Reference number: S19663; MUID:92085276
A;Accession: S19663
A;Molecule type: mRNA
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 SRDSSGIHVV 11
           |||||| |||
Db      89 SRDSSGNHVV 98
```

RESULT 3
B96635
hypothetical protein T7P1.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: B96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <STO>
A;Cross-references: GB:AE005173; NID:g6751686; PIDN:AAF27669.1; GSPDB:GN00141
C;Genetics:
A;Gene: T7P1.10
A;Map position: 1
C;Superfamily: Arabidopsis thaliana zinc transporter ZIP1

Query Match 74.5%; Score 41; DB 2; Length 389;
Best Local Similarity 63.6%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 GSRDSSGIHVV 11
           |  || |||:|
Db     166 GEEDSGGIHIV 176
```

RESULT 4
L3HUSH
Ig lambda chain V-III region (Sh) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C;Accession: A01980
itani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A;Reference number: A92057; MUID:70166723
A;Accession: A01980
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Note: the sequence of the C region is also given
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
F;21-86/Disulfide bonds: #status experimental

Query Match 70.9%; Score 39; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 SRDSSGIHVV 11
           |||||| ||:
Db      88 SRDSSGKHVL 97
```

RESULT 5
S25740
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25740
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162
A;Accession: S25740
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-190 <COM>
A;Cross-references: EMBL:X57804; NID:g33705; PIDN:CAA40942.1; PID:g33706
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;105-173/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 190;
Best Local Similarity 80.0%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 SRDSSGIHVV 11
           |||||| |:|
Db      65 SRDSSGNHLV 74
```

RESULT 6
T49426
Type 2C Protein Phosphatase related protein [imported] - Neurospora crassa
N;Alternate names: protein B17C10.70
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 17-Nov-2000
C;Accession: T49426
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49426
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-622 <SCH>
A;Cross-references: EMBL:AL355926; GSPDB:GN00116; NCSP:B17C10.70
A;Experimental source: BAC clone B17C10; strain OR74A
C;Genetics:
A;Gene: NCSP:B17C10.70
A;Map position: 6
A;Introns: 239/2
C;Superfamily: Arabidopsis thaliana hypothetical protein F20M13.80

Query Match 70.9%; Score 39; DB 2; Length 622;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GSRDSSGIH 9
           |:|||| |
Db      63 GARDSSGTH 71
```

RESULT 7
C89771
Immunoglobulin G binding protein A precursor [imported] - Staphylococcus aureus (stra
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89771
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:39:17 ; Search time 29.47 Seconds
(without alignments)
14.452 Million cell updates/sec

Title: US-09-780-035-14
Perfect score: 55
Sequence: 1 GSRDSSGIHVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	70.9	108	1	LV3A_HUMAN	P01714 homo sapien
2	38	69.1	508	1	SPA2_STAAU	P38507 staphylococ
3	38	69.1	524	1	SPA1_STAAU	P02976 staphylococ
4	36	65.5	109	1	PTHP_CHLTR	O84341 chlamydia t
5	35	63.6	136	1	MCH_METTO	Q9rpw3 methylococc
6	35	63.6	316	1	THER_BACTH	P00800 bacillus th
7	35	63.6	429	1	CBPX_ORYSA	P52712 oryza sativ
8	35	63.6	481	1	UGDH_CAEEL	Q19905 caenorhabdi
9	35	63.6	527	1	NPRE_BACBR	P43263 bacillus br
10	35	63.6	551	1	NPRS_BACST	P43133 bacillus st
11	35	63.6	576	1	MUTL_CHLTR	O84579 chlamydia t
12	35	63.6	610	1	DOPO_BOVIN	P15101 bos taurus
13	35	63.6	619	1	VAL1_YEAST	P38085 saccharomyc
14	35	63.6	620	1	DOPO_RAT	Q05754 rattus norv
15	35	63.6	633	1	PARE_MYCGE	P47445 mycoplasma
16	35	63.6	648	1	VP3_BPPH6	P11129 bacteriopha
17	34	61.8	258	1	EXUR_ECOLI	P42608 escherichia
18	34	61.8	273	1	DAPB_METTH	O26891 methanobact
19	34	61.8	488	1	HH1R_CAVPO	P31389 cavia porce
20	34	61.8	517	1	SEST_CAEEL	Q9n4d6 caenorhabdi
21	34	61.8	639	1	GYRB_HALSQ	P21558 haloferax s
22	34	61.8	687	1	DSPP_RAT	Q62598 rattus norv
23	34	61.8	1173	1	TSP1_XENLA	P35448 xenopus lae
24	34	61.8	1477	1	NX1A_HUMAN	Q9ulb1 homo sapien
25	34	61.8	1514	1	NX1A_RAT	Q63372 rattus norv
26	34	61.8	1530	1	NX1A_BOVIN	Q28146 bos taurus
27	34	61.8	2895	1	HYDP_DROME	P54592 drosophila
28	33	60.0	155	1	FGF2_XENLA	P12226 xenopus lae
29	33	60.0	259	1	EXUR_ERWCH	Q9x9e0 erwinia chr
30	33	60.0	285	1	MENB_ECOLI	P27290 escherichia
31	33	60.0	285	1	MENB_HAEIN	P44960 haemophilus
32	33	60.0	413	1	IF49_TOBAC	Q40471 nicotiana t
33	33	60.0	413	1	IF4Z_TOBAC	Q40468 nicotiana t
34	33	60.0	562	1	NPRM_BACME	Q00891 bacillus me
35	33	60.0	566	1	NPRE_BACCE	P05806 bacillus ce
36	33	60.0	590	1	NPRE_PAEPO	P29148 paenibacill
37	33	60.0	746	1	GYP7_YEAST	P48365 saccharomyc
38	33	60.0	810	1	SYFB_SYNY3	P74296 synechocyst
39	33	60.0	2124	1	PGCA_RAT	P07897 rattus norv
40	32.5	59.1	318	1	BST1_HUMAN	Q10588 homo sapien
41	32	58.2	206	1	ADEN_ADEG1	P42672 avian adeno
42	32	58.2	243	1	YJFH_ECOLI	P39290 escherichia
43	32	58.2	260	1	VBR1_ICMV	Q08595 indian cass
44	32	58.2	285	1	MENB_PASMU	Q9clv5 pasteurella
45	32	58.2	285	1	RL2_MYCGE	P47400 mycoplasma

ALIGNMENTS

RESULT 1
LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges.";
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01980; L3HUSH.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 21 86
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.66;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| ||:
Db 88 SRDSSGKHVL 97

RESULT 2
SPA2_STAAU
ID SPA2_STAAU STANDARD; PRT; 508 AA.
AC P38507;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Immunoglobulin G binding protein A precursor (IGG binding protein A).
GN SPA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=COWAN 1 / NCTC 8530;
RX   MEDLINE=88112878; PubMed=2828190;
RA   Shuttleworth H.L., Duggleby C.J., Jones S.A., Atkinson T.,
RA   Minton N.P.;
RT   "Nucleotide sequence analysis of the gene for protein A from
RT   Staphylococcus aureus Cowan 1 (NCTC8530) and its enhanced expression
RT   in Escherichia coli.";
RL   Gene 58:283-295(1987).
RN   [2]
RP   PARTIAL SEQUENCE.
RC   STRAIN=COWAN 1 / NCTC 8530;
RX   MEDLINE=78023926; PubMed=913410;
RA   Sjoedahl J.;
RT   "Structural studies on the four repetitive Fc-binding regions in
RT   protein A from Staphylococcus aureus.";
RL   Eur. J. Biochem. 78:471-490(1977).
RN   [3]
RP   STRUCTURE BY NMR OF 211-270.
RX   MEDLINE=93003122; PubMed=1390743;
RA   Gouda H., Torigoe H., Saito A., Sato M., Arata Y., Shimada I.;
RT   "Three-dimensional solution structure of the B domain of
RT   staphylococcal protein A: comparisons of the solution and crystal
RT   structures.";
RL   Biochemistry 31:9665-9672(1992).
RN   [4]
RP   STRUCTURE BY NMR OF 37-92.
RX   MEDLINE=97110349; PubMed=8952510;
RA   Starovasnik M.A., Skelton N.J., O'Connell M.P., Kelley R.F.,
RA   Reilly D., Fairbrother W.J.;
RT   "Solution structure of the E-domain of staphylococcal protein A.";
RL   Biochemistry 35:15558-15569(1996).
RN   [5]
RP   STRUCTURE BY NMR OF 212-269.
RX   MEDLINE=97467196; PubMed=9325113;
RA   Tashiro M., Tejero R., Zimmerman D.E., Celda B., Nilsson B.,
RA   Montelione G.T.;
RT   "High-resolution solution NMR structure of the Z domain of
RT   staphylococcal protein A.";
RL   J. Mol. Biol. 272:573-590(1997).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
CC   -!- DOMAIN: THE N-TERMINAL HALF CONTAINS THE IG-BINDING REGION
CC       WHILST THE C-TERMINAL HALF IS THE CELL-WALL-BINDING DOMAIN.
CC   -!- MISCELLANEOUS: IMPORTANT IMMUNODIAGNOSTIC REAGENT BECAUSE OF ITS
CC       ABILITY TO BIND THE FC FRAGMENT OF A WIDE RANGE OF MAMMALIAN
CC       IMMUNOGLOBULINS.
CC   -!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
CC       IN THE REGION OF THE MEMBRANE ANCHOR.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M18264; AAA26677.1; -.
DR   PIR; A29605; A29605.
DR   PDB; 1BDC; 11-JAN-97.
DR   PDB; 1BDD; 11-JAN-97.
DR   PDB; 1EDI; 01-APR-97.
DR   PDB; 1EDJ; 01-APR-97.
DR   PDB; 1EDK; 01-APR-97.
DR   PDB; 1EDL; 01-APR-97.
DR   PDB; 2SPZ; 21-APR-00.
DR   InterPro; IPR003132; B_domain.
DR   InterPro; IPR001899; Gram_pos_anchor.
DR   InterPro; IPR002482; LysM.
DR   Pfam; PF02216; B; 5.
DR   Pfam; PF00746; Gram_pos_anchor; 1.
DR   Pfam; PF01476; LysM; 1.
DR   SMART; SM00257; LysM; 1.
DR   PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
KW   IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
KW   3D-structure.
FT   SIGNAL       1     36       POTENTIAL.
FT   CHAIN       37    508       IMMUNOGLOBULIN G BINDING PROTEIN A.
FT   DOMAIN      37    482       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   483    503       POTENTIAL.
FT   DOMAIN     504    508       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      37    332       5 X 57 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT      37    100       1-1.
FT   REPEAT     101    158       1-2.
FT   REPEAT     159    216       1-3.
FT   REPEAT     217    274       1-4.
FT   REPEAT     275    332       1-5.
FT   DOMAIN     333    408       12 X 8 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT     333    340       2-1.
FT   REPEAT     341    348       2-2.
FT   REPEAT     349    356       2-3.
FT   REPEAT     357    364       2-4.
FT   REPEAT     365    372       2-5.
FT   REPEAT     373    380       2-6.
FT   REPEAT     381    388       2-7.
FT   REPEAT     389    396       2-8.
FT   REPEAT     397    405       2-9.
FT   REPEAT     406    413       2-10.
FT   REPEAT     414    421       2-11.
FT   REPEAT     422    429       2-12.
FT   DOMAIN     474    479       CONSERVED IN GRAM-POSITIVE COCCI SURFACE
FT                               PROTEINS.
FT   CONFLICT   273    273       K -> D (IN REF. 2).
SQ   SEQUENCE   508 AA;  55439 MW;  E78C538D4B5E88F5 CRC64;


  Query Match             69.1%;  Score 38;  DB 1;  Length 508;
  Best Local Similarity   54.5%;  Pred. No. 6.1;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GSRDSSGIHVV 11
           |  | :|:|||
Db     407 GKEDGNGVHVV 417


RESULT   3
SPA1_STAAU
ID   SPA1_STAAU     STANDARD;      PRT;   524 AA.
AC   P02976;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Immunoglobulin G binding protein A precursor (IGG binding protein A).
GN   SPA.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC 8325-4;
RX   MEDLINE=84111639; PubMed=6319407;
RA   Uhlen M., Guss B., Nilsson B., Gatenbeck S., Philipson L.,
RA   Lindberg M.;
RT   "Complete sequence of the staphylococcal gene encoding protein A. A
RT   gene evolved through multiple duplications.";
RL   J. Biol. Chem. 259:1695-1702(1984).
RN   [2]
RP   REVISIONS.
RC   STRAIN=8325-4;
RA   Uhlen M., Guss B., Nilsson B., Gatenbeck S., Philipson L.,
RA   Lindberg M.;
RL   J. Biol. Chem. 259:13628-13628(1984).
RN   [3]
RP   SEQUENCE OF 1-186 FROM N.A.
RC   STRAIN=8325-4;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:38:43 ; Search time 107.96 Seconds
(without alignments)
17.626 Million cell updates/sec

Title: US-09-780-035-14
Perfect score: 55
Sequence: 1 GSRDSSGIHVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

T[redacted] number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

[redacted] Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	74.5	386	10	Q9FPW7	Q9fpw7 thlaspi cae
2	41	74.5	389	10	Q9C957	Q9c957 arabidopsis
3	41	74.5	422	10	Q93XE7	Q93xe7 thlaspi cae
4	40	72.7	458	17	Q96Y71	Q96y71 sulfolobus
5	39	70.9	639	2	O52165	O52165 mycoplasma
6	38	69.1	107	4	Q9NSD6	Q9nsd6 homo sapien
7	38	69.1	190	2	Q53760	Q53760 staphylococ
8	38	69.1	450	16	Q99XA2	Q99xa2 staphylococ
9	38	69.1	454	2	Q53759	Q53759 staphylococ
10	38	69.1	472	2	Q53779	Q53779 staphylococ
11	38	69.1	492	2	Q56193	Q56193 staphylococ
12	38	69.1	573	2	Q56192	Q56192 staphylococ
13	38	69.1	666	2	Q53833	Q53833 staphylococ
14	38	69.1	747	2	Q53832	Q53832 staphylococ
15	37	67.3	374	10	O04089	O04089 arabidopsis
16	37	67.3	985	5	Q17341	Q17341 caenorhabdi
17	37	67.3	1786	5	Q17344	Q17344 caenorhabdi
18	37	67.3	1809	5	Q17487	Q17487 caenorhabdi
19	37	67.3	1815	5	Q17488	Q17488 caenorhabdi
20	37	67.3	1867	5	Q17486	Q17486 caenorhabdi
21	37	67.3	2039	5	Q17489	Q17489 caenorhabdi
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24	36	65.5	333	9	Q98813	Q98813 bacteriopha
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27	35	63.6	170	13	Q9I9A1	Q9i9a1 gallus gall
28	35	63.6	176	5	O17529	O17529 caenorhabdi
29	35	63.6	200	8	Q9MJQ1	Q9mjq1 podospora c
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31	35	63.6	232	8	Q9MJQ4	Q9mjq4 podospora c
32	35	63.6	243	8	Q02672	Q02672 podospora a
33	35	63.6	281	16	O84139	O84139 chlamydia t
34	35	63.6	298	5	Q9VIC5	Q9vic5 drosophila
35	35	63.6	492	4	Q9BX61	Q9bx61 homo sapien
36	35	63.6	501	5	O76254	O76254 onchocerca
37	35	63.6	501	5	Q9TY54	Q9ty54 onchocerca
38	35	63.6	528	6	Q28094	Q28094 bos taurus
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40	35	63.6	573	5	Q22842	Q22842 caenorhabdi
41	35	63.6	574	11	O70513	O70513 rattus norv
42	35	63.6	597	6	Q9TVD1	Q9tvd1 bos taurus
43	35	63.6	610	6	Q9XTA0	Q9xta0 equus cabal
44	35	63.6	629	17	Q97B91	Q97b91 thermoplasm
45	35	63.6	1165	5	Q962L9	Q96219 plasmodium

ALIGNMENTS

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Q9FPW7
ID Q9FPW7 PRELIMINARY; PRT; 386 AA.
AC Q9FPW7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE ZN TRANSPORTER ZNT4.
GN ZNT4.
OS Thlaspi caerulescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Thlaspi.
OX NCBI_TaxID=107243;
RN [1]
RP SEQUENCE FROM N.A.
RA Letham D.L.D., Pence N.S., Kochian L.V.;
RT "Identification and characterization of multiple members of the ZIP
RT metal transport family from the Zn/Cd hyperaccumulator, Thlaspi
RT caerulescens.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF292370; AAG44953.1; -.
SQ SEQUENCE 386 AA; 40745 MW; D979B4A1563D93BF CRC64;

Query Match 74.5%; Score 41; DB 10; Length 386;
Best Local Similarity 63.6%; Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSRDSSGIHVV 11
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Db 169 GEEDSGGIHIV 179

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Q9C957
ID Q9C957 PRELIMINARY; PRT; 389 AA.
AC Q9C957;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PUTATIVE IRON-REGULATED TRANSPORTER.
GN   T7P1.10.
OS   Arabidopsis thaliana (Mouse-ear cress).
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OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
DR   EMBL; AC018908; AAG51647.1; -.
DR   InterPro; IPR002395; Kininogen.
DR   InterPro; IPR003689; Zip.
DR   Pfam; PF02535; Zip; 1.
DR   PRINTS; PR00334; KININOGEN.
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Db     166 GEEDSGGIHIV 176
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AC   Q93XE7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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GN   ZNT2.
OS   Thlaspi caerulescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Thlaspi.
OX   NCBI_TaxID=107243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=ROOT;
RA   Assuncao A.G.L., da Costa Martins P., de Folter S., Vooijs R.,
RA   Schat H., Aarts M.G.M.;
RT   "Elevated expression of metal transporter genes in three accessions of
RT   the metal hyperaccumulator Thlaspi caerulescens.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF275752; AAK69430.1; -.
SQ   SEQUENCE   422 AA;  44968 MW;  874B878BDD599AA6 CRC64;
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Db     205 GEEDSGGIHIV 215
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE D-LACTATE DEHYDROGENASE.
GN   ST2295.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000989; BAB67406.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   458 AA;  51003 MW;  DEC38835D018B86F CRC64;
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Qy       2 SRDSSGIHVV 11
           | || |||||
Db     138 SHDSGGIHVV 147
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AC   O52165;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TOPOISOMERASE IV SUBUNIT (TOPOISOMERASE IV SUBUNIT E).
GN   PARE.
OS   Mycoplasma hominis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2098;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PG21;
RX   MEDLINE=98353329; PubMed=9687401;
RA   Bebear C.M., Charron A., Bove J.M., Bebear C., Renaudin J.;
RT   "Cloning and nucleotide sequences of the topoisomerase IV parC and
RT   parE genes of Mycoplasma hominis.";
RL   Antimicrob. Agents Chemother. 42:2024-2031(1998).
RN   [2]
RP   SEQUENCE OF 403-501 FROM N.A.
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:24:30 ; Search time 49.09 Seconds
(without alignments)
5.473 Million cell updates/sec

Title: US-09-780-035-14
Perfect score: 55
Sequence: 1 GSRDSSGIHVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	76.4	97	2	US-08-665-202-35	Sequence 35, Appl
2	42	76.4	109	2	US-08-652-816A-16	Sequence 16, Appl
3	42	76.4	278	4	US-09-260-527-3	Sequence 3, Appli
4	42	76.4	280	4	US-09-260-527-1	Sequence 1, Appli
5	42	76.4	309	4	US-09-079-029-9	Sequence 9, Appli
6	42	76.4	312	4	US-09-079-029-10	Sequence 10, Appl
7	36	65.5	316	3	US-08-682-643-4	Sequence 4, Appli
8	36	65.5	409	2	US-09-031-485-15	Sequence 15, Appl
9	36	65.5	409	2	US-08-847-429A-15	Sequence 15, Appl
10	36	65.5	409	3	US-09-065-474-15	Sequence 15, Appl
11	36	65.5	1745	2	US-09-031-485-33	Sequence 33, Appl
12	36	65.5	1745	2	US-08-847-429A-33	Sequence 33, Appl
13	36	65.5	1745	3	US-09-065-474-33	Sequence 33, Appl
14	35	63.6	11	2	US-08-350-260A-349	Sequence 349, App
15	35	63.6	11	2	US-08-350-260A-430	Sequence 430, App
16	35	63.6	67	2	US-08-273-146-67	Sequence 67, Appl
17	35	63.6	316	1	US-08-038-932B-1	Sequence 1, Appli
18	35	63.6	316	1	US-08-656-349-1	Sequence 1, Appli
19	35	63.6	316	4	US-09-104-623A-5	Sequence 5, Appli
20	34	61.8	11	2	US-08-350-260A-516	Sequence 516, App
21	34	61.8	11	2	US-08-350-260A-522	Sequence 522, App
22	33	60.0	285	3	US-09-058-489-12	Sequence 12, Appl
23	33	60.0	566	1	US-08-415-823-4	Sequence 4, Appli
24	33	60.0	566	2	US-09-086-662-4	Sequence 4, Appli
25	33	60.0	15281	2	US-08-471-119A-2	Sequence 2, Appli
26	32.5	59.1	318	1	US-08-537-942A-1	Sequence 1, Appli
27	32.5	59.1	318	4	US-08-997-252A-1	Sequence 1, Appli
28	32.5	59.1	318	4	US-09-517-739-1	Sequence 1, Appli
29	32	58.2	11	2	US-08-350-260A-342	Sequence 342, App
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31	32	58.2	106	4	US-09-240-274-50	Sequence 50, Appl
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36	32	58.2	169	2	US-08-926-922-12	Sequence 12, Appl
37	32	58.2	169	3	US-09-253-682-12	Sequence 12, Appl
38	32	58.2	169	4	US-09-527-657-12	Sequence 12, Appl
39	32	58.2	206	4	US-09-171-461-13	Sequence 13, Appl
40	32	58.2	319	3	US-08-682-643-3	Sequence 3, Appli
41	32	58.2	405	4	US-09-347-801-20	Sequence 20, Appl
42	32	58.2	511	2	US-08-271-397-2	Sequence 2, Appli
43	32	58.2	511	4	US-08-469-191-2	Sequence 2, Appli
44	32	58.2	511	5	PCT-US91-07280-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 35, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  97 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-35


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RESULT   2
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; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
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;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-652-816A-16

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; Patent No. 6228599
; GENERAL INFORMATION:
;  APPLICANT: Knox, J.P.
;  APPLICANT: Mikkelsen, J.D.
;  APPLICANT: Willats, W. G.
;  TITLE OF INVENTION: ANTIBODY
;  FILE REFERENCE: DYOU19.001AUS
;  CURRENT APPLICATION NUMBER: US/09/260,527A
;  CURRENT FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 7
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;   LENGTH: 278
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;   OTHER INFORMATION: from a naive phage display library known as the
;   OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
;   OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

  Query Match             76.4%;  Score 42;  DB 4;  Length 278;
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Qy       2 SRDSSGIHVV 11
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Db     241 SRDSSGNHVV 250


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; Patent No. 6228599
; GENERAL INFORMATION:
;  APPLICANT: Knox, J.P.
;  APPLICANT: Mikkelsen, J.D.
;  APPLICANT: Willats, W. G.
;  TITLE OF INVENTION: ANTIBODY
;  FILE REFERENCE: DYOU19.001AUS
;  CURRENT APPLICATION NUMBER: US/09/260,527A
;  CURRENT FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
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;   OTHER INFORMATION: phage display library known as the Synthetic scFv
;   OTHER INFORMATION: Library (#1) from the Centre for Protein
;   OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

  Query Match             76.4%;  Score 42;  DB 4;  Length 280;
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 10:57:38 ; Search time 28.87 Seconds
(without alignments)
23.084 Million cell updates/sec

Title: US-09-780-035-9
Perfect score: 37
Sequence: 1 TGYYIH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 36243

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	100.0	6	22	AAB50794	Murine antibody S2
2	37	100.0	6	22	AAG65299	Anti-IL-18 antibod
3	29	78.4	5	20	AAW95252	Anti-progesterone
4	29	78.4	5	22	AAB86299	Murine derived ant
5	28	75.7	5	21	AAB21360	Rat antibody 2C10
6	27	73.0	5	16	AAR76079	MAb 55.1 heavy cha
7	26	70.3	5	18	AAW27347	CDR1 from murine a
8	26	70.3	6	18	AAW42309	Biotinylated cross
9	25	67.6	5	21	AAB26978	Rat antibody 14B7
10	24	64.9	5	17	AAR95324	Anti-thyroid perox
11	23	62.2	5	20	AAY52749	Humanised ATR-5 H
12	23	62.2	5	21	AAB07960	CDR1 sequence from
13	23	62.2	6	19	AAW87188	Peptide determined
14	23	62.2	6	19	AAW87190	Peptide determined
15	21	56.8	5	18	AAW19193	Isoelectric point
16	21	56.8	5	19	AAW87109	Peptide determined
17	21	56.8	5	19	AAW87110	Peptide determined
18	21	56.8	5	19	AAW70923	CDR1 of the heavy
19	21	56.8	5	20	AAW93178	Nerve related pept
20	21	56.8	5	22	AAB86043	H. pylori catalase
21	21	56.8	5	22	AAB86075	H. pylori catalase
22	21	56.8	6	14	AAR37396	Peptide for treati
23	21	56.8	6	18	AAW19190	Isoelectric point
24	21	56.8	6	20	AAW93177	Nerve related pept
25	21	56.8	6	21	AAY50630	Alpha1-proteinase
26	20	54.1	4	18	AAW25216	Synthetic peptide
27	20	54.1	4	19	AAW62358	Peptide exhibiting
28	20	54.1	5	17	AAR91722	NAP subsequence.
29	20	54.1	5	17	AAR91723	NAP subsequence.
30	20	54.1	5	18	AAW25215	Synthetic peptide
31	20	54.1	5	19	AAW39863	Heavy chain CDR1 o
32	20	54.1	5	20	AAY49216	Seq ID No: 13 of U
33	20	54.1	5	20	AAY30441	Nematode extracted
34	20	54.1	5	20	AAY30442	Nematode extracted
35	20	54.1	5	21	AAB15326	NAP domain fragmen
36	20	54.1	5	21	AAB15327	NAP domain fragmen
37	20	54.1	5	22	AAM51295	Anti-HIV peptide w
38	20	54.1	5	22	AAM51357	Anti-HIV peptide w
39	20	54.1	5	22	AAM51419	Tea opioid peptide
40	20	54.1	5	22	AAB81027	Gluteomorphin pept
41	20	54.1	6	13	AAR25076	Opioid peptide fro
42	20	54.1	6	14	AAR37395	Peptide for treati
43	20	54.1	6	17	AAR92553	VLA-4 binding pept
44	20	54.1	6	17	AAR92606	VLA-4 binding pept
45	20	54.1	6	22	AAM51308	Anti-HIV peptide w

ALIGNMENTS

RESULT 1
AAB50794
ID AAB50794 standard; Protein; 6 AA.
XX
AC AAB50794;
XX
DT 21-MAR-2001 (first entry)
XX
DE Murine antibody S2C6 heavy chain variable region CDR1.
XX
KW Mouse; antibody; S2C6; heavy chain variable region; CD40; cancer;
KW inflammatory disease; immune system disorder; CDR;
KW complementarity determining region.
XX
OS Mus musculus.
XX
PN WO200075348-A1.
XX
PD 14-DEC-2000.
XX
PF 08-JUN-2000; 2000WO-US15749.
XX
PR 08-JUN-1999; 99US-0328296.
XX
PA (SEAT-) SEATTLE GENETICS INC.
XX
PI Siegall CB, Wahl AF, Francisco JA, Fell HP;
XX
DR WPI; 2001-071080/08.
XX
PT Anti-CD40 antibodies which immunospecifically bind CD40, useful for
PT prevention and treatment of cancer, inflammatory diseases and disorders
PT or deficiencies of immune system -
XX

PS Claim 1; Page 88; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC anti-CD40 antibodies. These can be used in the treatment of cancer and
CC inflammatory and immune system diseases, including systemic lupus
CC erythematosus, scleroderma, inflammatory myositis, Sjogren's syndrome,
CC mixed connective tissue disease, rheumatoid arthritis, multiple
CC sclerosis, inflammatory bowel disease, acute respiratory distress
CC syndrome, pulmonary inflammation, osteoporosis, delayed type
CC hypersensitivity, asthma, primary biliary cirrhosis and idiopathic
CC thrombocytopaenic purpura.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 37; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 1 tgyyih 6

RESULT 2
AAG65299
ID AAG65299 standard; protein; 6 AA.
XX
AC AAG65299;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain CDR1 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 25; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain CDR1 fragment.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 37; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYYIH 6
||||||
Db 1 tgyyih 6

RESULT 3
AAW95252
ID AAW95252 standard; peptide; 5 AA.
XX
AC AAW95252;
XX
DT 11-MAR-1999 (first entry)
XX
DE Anti-progesterone antibody Vh region (clone 1578/p1) CDR H1 sequence.
XX
KW ARM; protein selection; display; cell free system; genetic information;
KW reverse transcription; single-chain antibody; RT-PCR; primer; drug;
KW antibody-ribosome-mRNA complex; antibody engineering; progesterone;
KW testosterone; human
XX
OS Homo sapiens.
XX
PN WO9854312-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-GB01564.
XX
PR 28-FEB-1998; 98GB-0004195.
PR 28-MAY-1997; 97GB-0010829.
PR 26-NOV-1997; 97GB-0024850.
XX
PA (BABR-) BABRAHAM INST.
XX
PI He M, Taussig MJ;
XX
DR WPI; 1999-059832/05.
XX
PT In vitro display and evolution of proteins - by transcription and
PT translation of DNA in a cell free system, selection and recovery of
PT complexes and RT-PCR on RNA bound to ribosomes
XX
PS Example 13; Fig 19; 62pp; English.
XX
CC The invention relates to methods for the display and selection of
CC proteins or peptides and for recovery of the genetic material encoding
CC them. One method comprises (a) transcription and translation of DNA in a
CC cell free system such that complexed particles are formed, each
CC comprising at least one individual nascent protein or peptide or other
CC DNA expression product associated with one or more ribosomes and the
CC specific mRNA encoding the protein or peptide; (b) contacting the
CC complexed particles with a ligand, antigen, antibody or other agent in
CC order to select particles through binding to the protein or peptide
CC product; and (c) recovering the genetic information encoding the protein
CC or peptide as DNA by RT-PCR carried out on the mRNA while the latter
CC remains bound to the complexed particle. The steps of display, selection
CC and recovery can be repeated in consecutive cycles. The method is
CC exemplified using single-chain antibody constructs as antibody-ribosome-
CC mRNA complexes (ARMs). Methods in which the DNA is produced by RT-PCR,

CC methods for making antibodies of human, mouse or rat are also provided.
CC The methods can be used for the display and selection of single chain
CC antibody fragments from libraries, antibody engineering, selection of
CC human antibodies and selection of proteins from mRNA libraries. They can
CC also be used to select ligands for combining sites or receptors, such
CC ligands having potential uses as drugs or therapies. By carrying out the
CC RT-PCR recovery stop directly on the intact ribosome complex without
CC prior dissociation to release the mRNA maximal efficiency and
CC sensitivity can be obtained. Peptides AAW95247 to AAW95271 represent
CC sequences of human anti-progesterone and anti-testosterone antibodies
CC isolated from an immunised transgenic mouse by ARM display.
XX
SQ Sequence 5 AA;

Query Match 78.4%; Score 29; DB 20; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYYIH 6
|||:|
Db 1 gyymh 5

RESULT 4
AAB86299
ID AAB86299 standard; peptide; 5 AA.
XX
AC AAB86299;
XX
DT 13-SEP-2001 (first entry)
XX
DE Murine derived antibody Wue-1 heavy chain variable region CDR-1.
XX
KW Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
KW immunomodulatory; cognate antigen identification; autoimmune disease;
KW tumor; multiple myeloma; lymphoma; plastocytoma; CDR-1.
XX
OS Mus sp.
XX
PN DE19962583-A1.
XX
PD 28-JUN-2001.
XX
PF 23-DEC-1999; 99DE-1062583.
XX
PR 23-DEC-1999; 99DE-1062583.
XX
PA (MUEL/) MUELLER-HERMELINK H K.
PA (GREI/) GREINER A.
XX
PI Mueller-Hermelink HK, Greiner A;
XX
DR WPI; 2001-426596/46.
XX
PT New antibodies specific for plasma cells, useful for treatment and
PT diagnosis of autoimmune diseases and plasma cell tumors -
XX
PS Claim 1; Page 11; 18pp; German.
XX
CC This invention describes novel antibodies (Ab) in which the variable
CC region (VR) of at least one chain and/or the VR of at least one heavy
CC chain includes at least one of 7 specified sequences, or fragments of
CC these sequences, or contain at least one light chain and/or heavy
CC chain encoded by specific nucleic acid sequences (I) and (II),
CC reproduced, or their fragments. The products of the invention have
CC antitumor and immunomodulatory activity. Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plastocytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursor stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional
CC chemotherapeutic agents. This sequence represents the Wue-1 antibody
CC variable region heavy chain complementarity determining region CDR-1
CC fragment described in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 78.4%; Score 29; DB 22; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYYIH 6
|||:|
Db 1 gyymh 5

RESULT 5
AAB21360
ID AAB21360 standard; Peptide; 5 AA.
XX
AC AAB21360;
XX
DT 25-JAN-2001 (first entry)
XX
DE Rat antibody 2C10 heavy chain variable region CDR I.
XX
KW Rat; antibody 2C10; antiarthritic; immunosuppressive; neuroprotective;
KW antiinflammatory; antipsoriatic; interleukin-18; IL-18;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
KW inflammatory bowel disease; complementarity determining region; CDR.
XX
OS Rattus norvegicus.
XX
PN WO200056771-A1.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07349.
XX
PR 19-MAR-1999; 99US-0125299.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
XX
DR WPI; 2000-628249/60.
DR N-PSDB; AAA99639.
XX
PT Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
PT antibody having high affinity and useful for treating IL-18 mediated
PT disorders such as multiple sclerosis, rheumatoid arthritis and
PT psoriasis -
XX
PS Disclosure; Fig 2; 64pp; English.
XX
CC The present sequence is complementarity determining region I (CDR I)
CC of the rat antibody 2C10 heavy chain variable region. The antibody has
CC high affinity for human interleukin-18 (IL-18) and is useful for treating
CC and diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as
CC multiple sclerosis, rheumatoid arthritis, type I or insulin dependent
CC diabetes, inflammatory bowel disease and psoriasis. Specific changes can
CC be introduced into the nucleotide sequences encoding the CDRs or
CC framework regions of the variable light chain and heavy chain peptides.
CC The resulting modified or fusion nucleic acid sequences can then be
CC introduced into a plasmid for expression.
XX
SQ Sequence 5 AA;

```
  Query Match             75.7%;  Score 28;  DB 21;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GYYIH 6
          ||| |
Db      1 gyyfh 5


RESULT   6
AAR76079
ID   AAR76079 standard; Peptide; 5 AA.
XX
AC   AAR76079;
XX
DT   21-NOV-1995  (first entry)
XX
DE   MAb 55.1 heavy chain CDR1.
XX
KW   Antigen binding structure; complementarity determining region; CDR;
KW   CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW   monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW   transgenic animal; transgenic plant; antibody engineering;
KW   humanized antibody; immunotoxin.
XX
OS   Mus sp.
XX
PN   WO9515382-A.
XX
PD   08-JUN-1995.
XX
PF   29-NOV-1994;   94WO-GB02610.
XX
PR   03-JUN-1994;   94GB-0011089.
PR   03-DEC-1993;   93GB-0024819.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Blakey DC,  Boot C,  Copley CG,  Hall SM,  Paterson DS;
PI   Rose MS,  Wright AF;
XX
DR   WPI; 1995-215262/28.
XX
PT   Antigen binding structures containing CDRs recognising the CA55.1
PT   antigen - produced by hybridomas and host cells, for use in the
PT   diagnosis and therapy of cancer
XX
CC   Claim 2; Page 96; 121pp; English.
CC
CC   An antigen binding structure is based on the CDRs (given in AAR76078-
CC   84) of the heavy and light chains of MAb 55.1 (ECACC 93081901),
CC   which recognises the colorectal tumor-associated antigen CA55.1.
CC   It is optionally humanized and in the form F(ab')2, F(ab)', Fab,
CC   Fv, scFv or V-min, and is produced in transgenic animals or plants.
XX
SQ   Sequence   5 AA;


  Query Match             73.0%;  Score 27;  DB 16;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 GYYIH 6
          ||:||
Db      1 gywih 5


RESULT   7
AAW27347
ID   AAW27347 standard; peptide; 5 AA.
XX
AC   AAW27347;
XX
```

```
DT   12-DEC-1997  (first entry)
XX
DE   CDR1 from murine anti-human IgE receptor antibody light chain.
XX
KW   Complementarity determining region; CDR1; murine; mouse; human;
KW   high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW   IgE; MAb; light chain; variable region; humanised; semi-chimeric;
KW   chimeric; treatment; prevention; disease; allergy.
XX
OS   Mus spp.
XX
PN   JP09191886-A.
XX
PD   29-JUL-1997.
XX
PF   19-JAN-1996;   96JP-0024816.
XX
PR   19-JAN-1996;   96JP-0024816.
XX
PA   (ASAK ) ASAHI BREWERIES LTD.
PA   (NIKK-) NIKKA WHISKEY KK.
PA   (TORI ) TORII YAKUHIN KK.
PA   (TSUR/) TSURA T.
XX
DR   WPI; 1997-429186/40.
XX
PT   Humanised, semi-chimeric and chimeric antibodies against human
PT   high-affinity IgE receptor  - useful medicinally and have low
PT   antigenicity in humans
XX
PS   Claim 1; Page 13; 26pp; Japanese.
XX
CC   The present complementarity determining region 1 (CDR1), which is
CC   from a murine, anti-human high affinity immunoglobulin E (IgE)
CC   receptor, monoclonal antibody (MAb) light chain variable region,
CC   can be used in the preparation of humanised or semi-chimeric
CC   anti-human high affinity IgE receptor MAb. The MAb can be used to
CC   treat or prevent diseases, specifically allergies, associated with
CC   the receptor. The humanised, semi-chimeric or chimeric MAb have
CC   very low antigenicity in humans.
XX
SQ   Sequence   5 AA;


  Query Match             70.3%;  Score 26;  DB 18;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 YYIH 6
          ||||
Db      2 yyih 5


RESULT   8
AAW42309
ID   AAW42309 standard; Peptide; 6 AA.
XX
AC   AAW42309;
XX
DT   08-APR-1998  (first entry)
XX
DE   Biotinylated cross-linked interleukin-8 6-mer peptide ligand 16.
XX
KW   Bacteriophage peptide library; peptide epitope; therapeutic target;
KW   variegated compound library; interleukin-8; IL-8.
XX
OS   Synthetic.
XX
PN   WO9735194-A2.
XX
PD   25-SEP-1997.
XX
PF   21-MAR-1997;   97WO-US04176.
```

XX
PR 21-MAR-1996; 96US-0622338.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Forster AC;
XX
DR WPI; 1997-480355/44.
XX
PT Identifying compounds which interact with target molecules - using
PT enantiomers of the target molecules and testing of enantiomers of
PT selected compounds.
XX
PS Disclosure; Fig 7; 89pp; English.
XX
CC 6-mer peptides AAW42294-309 are identified as ligands of a biotinylated,
CC cross-linked interleukin-8 (IL-8) target, using the method of the
CC invention. This novel method identifies compounds which interact with
CC a target molecule, and comprises contacting a screening molecule with
CC a variegated compound library, where the screening molecule comprises
CC solid target molecule, or the enantiomer if the target molecule is
CC chiral. Compounds which have a desired interaction with the target
CC molecule are selected, and the ability of their enantiomer to interact
CC with the target molecule is tested. Ligands for a target protein can be
CC identified by combining a D-enantiomer of a target protein (a D-target
CC protein), and a variegated compound library, and then selecting one or
CC more compounds from the library which have a desired binding interaction
CC with the D-target protein. The methods can be used for identifying
CC agonists or antagonists of targets such as receptors, enzymes, DNA
CC binding proteins or signal transduction proteins. The methods can
CC provide a structurally selective approach in addition to scoring for
CC interaction of functional groups. They provide a powerful selection
CC method that allows for the production of ligands with the same diversity
CC as peptides but with the greatly improved pharmacokinetic profiles needed
CC for drug activity.
XX
SQ Sequence 6 AA;

Query Match 70.3%; Score 26; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYIH 6
||||
Db 1 yyih 4

RESULT 9
AAB26978
ID AAB26978 standard; Peptide; 5 AA.
XX
AC AAB26978;
XX
DT 25-JAN-2001 (first entry)
XX
DE Rat antibody 14B7 heavy chain variable region CDR I.
XX
KW Rat; antibody 14B7; antiarthritic; immunosuppressive; neuroprotective;
KW antiinflammatory; antipsoriatic; interleukin-18; IL-18;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
KW inflammatory bowel disease; complementarity determining region; CDR.
XX
OS Rattus norvegicus.
XX
PN WO200056771-A1.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07349.
XX
PR 19-MAR-1999; 99US-0125299.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
XX
DR WPI; 2000-628249/60.
DR N-PSDB; AAA99655.
XX
PT Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
PT antibody having high affinity and useful for treating IL-18 mediated
PT disorders such as multiple sclerosis, rheumatoid arthritis and
PT psoriasis -
XX
PS Disclosure; Fig 6; 64pp; English.
XX
CC The present sequence is complementarity determining region I (CDR I)
CC of the rat antibody 14B7 heavy chain variable region. The antibody has
CC high affinity for human interleukin-18 (IL-18) and is useful for treating
CC and diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as
CC multiple sclerosis, rheumatoid arthritis, type I or insulin dependent
CC diabetes, inflammatory bowel disease and psoriasis. Specific changes can
CC be introduced into the nucleotide sequences encoding the CDRs or
CC framework regions of the variable light chain and heavy chain peptides.
CC The resulting modified or fusion nucleic acid sequences can then be
CC introduced into a plasmid for expression.
XX
SQ Sequence 5 AA;

Query Match 67.6%; Score 25; DB 21; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYIH 6
||:|
Db 2 yyvh 5

RESULT 10
AAR95324
ID AAR95324 standard; peptide; 5 AA.
XX
AC AAR95324;
XX
DT 24-OCT-1996 (first entry)
XX
DE Anti-thyroid peroxidase antibody clone SP1.2 heavy chain CDR1.
XX
KW Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR;
KW complementarity determining region; light; heavy chain; PCR;
KW polymerase chain reaction; antibody library; diversity; affinity;
KW immunospecificity; ds.
XX
OS Synthetic.
XX
PN WO9607754-A1.
XX
PD 14-MAR-1996.
XX
PF 01-SEP-1995; 95WO-US11235.
XX
PR 02-SEP-1994; 94US-0300386.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Burton DR, Lerner RA;
XX
DR WPI; 1996-171625/17.
XX
PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
PT gene CDR - useful for prodn. of Ig heavy and light chain
PT combinatorial antibody libraries

XX
PS Example 9C; Page 76; 125pp; English.
XX
CC AAR95324, AAR95325 and AAR99005 are heavy chain complementarity
CC determining regions (CDRs) 1, 2 and 3, respectively of an anti-thyroid
CC peroxidase (TPO) antibody clone SP1.2. Several anti-TPO clones were made
CC using mutagenic primers which induce mutations in the CDRs of the light
CC and heavy chain variable regions, the primers pref. mutate CDR3 of a
CC human Ig light chain. The mutagenic primers have sequences at their 3'
CC and 5' ends both capable of binding different framework regions linked
CC by a sequence 6 to 50 nucleotides long. Different immunoglobulins
CC produced using the primers may be used to produce antibody libraries
CC having diverse and novel immunospecificities and affinities. By using
CC mutagenic ONs an extremely large population of different randomised
CC binding sites can be created and use of the universal light chain
CC increases the number of combinations which yield functional
CC heterodimeric antibodies.
XX
SQ Sequence 5 AA;

Query Match 64.9%; Score 24; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYYIH 6
|:|:|
Db 1 ghymh 5

RESULT 11
AAY52749
ID AAY52749 standard; Peptide; 5 AA.
XX
AC AAY52749;
XX
DT 26-JAN-2000 (first entry)
XX
DE Humanised ATR-5 H chain V region CDR1.
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP01768.
XX
PR 03-APR-1998; 98JP-0091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Sato K, Adachi H, Yabuta N;
XX
DR WPI; 1999-620204/53.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment
PT of disseminated intravascular coagulation -
XX
PS Claim 11; Page 271; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
CC chains containing the variable region of the L chain of a mouse
CC monoclonal Ab recognising human tissue factor (hTF) and the constant
CC region of the L chain of a human Ab, the variable region being one of six
CC specified sequences (which are the L chain variable regions from mouse
CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
CC the treatment and prevention of thrombotic disease, especially of
CC disseminated intravascular coagulation (DIC). The humanised antibody has
CC the high hTF binding activity of the mouse monoclonal antibody but
CC greatly reduced immunogenicity. AAZ33001 to AAZ33091 and Y527007 to
CC AAY52767 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 5 AA;

Query Match 62.2%; Score 23; DB 20; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYIH 6
||:|
Db 2 yymh 5

RESULT 12
AAB07960
ID AAB07960 standard; peptide; 5 AA.
XX
AC AAB07960;
XX
DT 14-NOV-2000 (first entry)
XX
DE CDR1 sequence from an antibody with affinity for B7 molecules.
XX
KW Complementarity determining region; CDR; antibody; B7 molecule; B7-1;
KW B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;
KW inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;
KW insulitis; asthma; arthritis; inflammatory bowel disease; cancer;
KW inflammatory dermatitis; multiple sclerosis; transplant rejection;
KW proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;
KW thalassemia; aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Mus sp.
XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Disclosure; Page 29; 162pp; English.
XX
CC The present sequence represents a complementarity determining region
CC (CDR) 1 from the heavy chain of an murine antibody with having a
CC binding specificity to B7-1 molecules. The sequence is used to construct
CC humanized immunoglobulins, which comprise an antigen binding region of
CC non-human origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infectious
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes

CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 5 AA;

Query Match 62.2%; Score 23; DB 21; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YYIH 6
||:|
Db 2 yymh 5

RESULT 13
AAW87188
ID AAW87188 standard; peptide; 6 AA.
XX
AC AAW87188;
XX
DT 09-FEB-1999 (first entry)
XX
DE Peptide determined by the method of the invention.
XX
KW Amino acid determination; molecular mass; fragmentation spectrum;
KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
XX
OS Synthetic.
XX
PN GB2325465-A.
XX
PD 25-NOV-1998.
XX
PF 22-MAY-1998; 98GB-0011196.
XX
PR 22-MAY-1997; 97GB-0010582.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Prime SB, Townsend RR, Wedd NS;
XX
DR WPI; 1998-571195/49.
XX
PT Peptide sequence determination used in e.g. DNA cloning - by
PT comparing mass spectra of the unknown peptide with a library of
PT linear chain known peptide sequences
XX
PS Example 1; Page 20; 40pp; English.
XX
CC The invention relates to a method for determination of the amino acid
CC sequence of an unknown peptide. The method comprises (a) determining
CC the molecular mass and an experimental fragmentation spectrum for the
CC peptide; (b) comparing the experimental fragmentation spectrum of the
CC unknown peptide with a theoretical fragmentation spectra calculated for
CC a peptide library composed of all possible linear sequences of amino
CC acids having a total mass that corresponds to the molecular mass of the
CC unknown peptide; and (c) identifying a peptide in the library with a
CC theoretical fragmentation spectrum that most closely matches the
CC fragmentation spectrum of the unknown peptide. The method is useful in
CC DNA cloning, anti-body production, identification of recombinant
CC products, and the study of post-translational modifications. It allows
CC the sequence of unknown peptides or proteins with no sub-sequence
CC identity, to be characterised using mass spectrometry. Sequences
CC AAW87101 to AAW87364 represent a library of linear peptides constructed
CC to exemplify the method. The isoleucine residue in these peptides can be
CC replaced by leucine to construct another 264 linear peptides to be
CC included in the library.
XX
SQ Sequence 6 AA;

Query Match 62.2%; Score 23; DB 19; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYYIH 6
|| ||
Db 1 gyeih 5

RESULT 14
AAW87190
ID AAW87190 standard; peptide; 6 AA.
XX
AC AAW87190;
XX
DT 09-FEB-1999 (first entry)
XX
DE Peptide determined by the method of the invention.
XX
KW Amino acid determination; molecular mass; fragmentation spectrum;
KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
XX
OS Synthetic.
XX
PN GB2325465-A.
XX
PD 25-NOV-1998.
XX
PF 22-MAY-1998; 98GB-0011196.
XX
PR 22-MAY-1997; 97GB-0010582.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Prime SB, Townsend RR, Wedd NS;
XX
DR WPI; 1998-571195/49.
XX
PT Peptide sequence determination used in e.g. DNA cloning - by
PT comparing mass spectra of the unknown peptide with a library of
PT linear chain known peptide sequences
XX
PS Example 1; Page 20; 40pp; English.
XX
CC The invention relates to a method for determination of the amino acid
CC sequence of an unknown peptide. The method comprises (a) determining
CC the molecular mass and an experimental fragmentation spectrum for the
CC peptide; (b) comparing the experimental fragmentation spectrum of the
CC unknown peptide with a theoretical fragmentation spectra calculated for
CC a peptide library composed of all possible linear sequences of amino
CC acids having a total mass that corresponds to the molecular mass of the
CC unknown peptide; and (c) identifying a peptide in the library with a
CC theoretical fragmentation spectrum that most closely matches the
CC fragmentation spectrum of the unknown peptide. The method is useful in
CC DNA cloning, anti-body production, identification of recombinant
CC products, and the study of post-translational modifications. It allows
CC the sequence of unknown peptides or proteins with no sub-sequence
CC identity, to be characterised using mass spectrometry. Sequences
CC AAW87101 to AAW87364 represent a library of linear peptides constructed
CC to exemplify the method. The isoleucine residue in these peptides can be
CC replaced by leucine to construct another 264 linear peptides to be
CC included in the library.
XX
SQ Sequence 6 AA;

Query Match 62.2%; Score 23; DB 19; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 GYYIH 6
          | |||
Db      1 geyih 5


RESULT  15
AAW19193
ID   AAW19193 standard; peptide; 5 AA.
XX
AC   AAW19193;
XX
DT   06-AUG-1997  (first entry)
XX
DE   Isoelectric point marker peptide 52.
XX
KW   Label; fluorescent dye; isoelectric; point; pI; marker; focusing;
KW   fluorescence; capillary; stable.
XX
OS   Synthetic.
XX
PN   EP744614-A2.
XX
PD   27-NOV-1996.
XX
PF   29-MAR-1996;   96EP-0105113.
XX
PR   19-OCT-1995;   95JP-0271196.
PR   31-MAR-1995;   95JP-0076873.
XX
PA   (MOLE-) LAB MOLECULAR BIOPHOTONICS.
XX
PI   Kasai K,  Matsumoto H,  Shimura K,  Takamoto H;
XX
DR   WPI; 1997-001360/01.
XX
PT   Isoelectric point markers for isoelectric focusing - comprising
PT   fluorescence-labelled oligo:nucleotide(s)
XX
PS   Example; Page 11; 29pp; English.
XX
CC   The present peptide, when labelled with a fluorescent dye, can be
CC   used as an isoelectric point (pI) marker for isoelectric focusing
CC   with fluorescence. The dye is linked to the peptide's
CC   amino-terminal through an amide, thioamide, sulphonamide, urea,
CC   thiourea or urethane bond, and is rhodamine, fluorescein, cyanine,
CC   indocyanine, indocarbocyanine, pyronine, lucifer yellow,
CC   quinacrine, squarillium, coumarin, fluoroanthranil maleimide or
CC   anthracene. The marker can be used for capillary isoelectric
CC   focusing, and it is possible to construct peptide sets that cover
CC   a wide pI range and have good storage stability.
CC   The present peptide has a calculated pI value of 7.90.
XX
SQ   Sequence   5 AA;


  Query Match             56.8%;  Score 21;  DB 18;  Length 5;
  Best Local Similarity   75.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 YYIH 6
          || |
Db      1 yyyh 4


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Job time: 58 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:03:09 ; Search time 28.81 Seconds
(without alignments)
15.422 Million cell updates/sec

Title: US-09-780-035-11
Perfect score: 20
Sequence: 1 KEGA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 9580

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	4	22	AAG65301	Anti-IL-18 antibod
2	16	80.0	4	12	AAR13812	Factor Xa substrat
3	16	80.0	4	19	AAY20704	Human neurofilamen
4	16	80.0	4	19	AAW81781	Human HE4 epitope
5	16	80.0	4	22	AAB62145	P. falciparum FCR3
6	15	75.0	4	21	AAY90390	Tumour necrosis fa
7	13	65.0	3	19	AAW56198	Anti-inflammatory
8	13	65.0	4	17	AAW05773	Presenilin-1-1 res
9	12	60.0	4	5	AAP40366	Sequence of inhibi
10	12	60.0	4	13	AAR23938	Lactoferrin-introd
11	12	60.0	4	16	AAR75498	C5a receptor-antag
12	12	60.0	4	16	AAR75499	C5a receptor-antag
13	12	60.0	4	18	AAW27455	Beta-endorphin C-t
14	12	60.0	4	18	AAW27456	Beta-endorphin C-t
15	12	60.0	4	18	AAW27457	Beta-endorphin C-t
16	12	60.0	4	18	AAW24497	Immobilised fluore
17	12	60.0	4	19	AAW64563	Tetrapeptide used
18	12	60.0	4	19	AAW17399	Acetyl-Lys-D-Lys-S
19	12	60.0	4	20	AAY42628	Murine melanoma an
20	12	60.0	4	20	AAY31051	Non-crosslinked pr
21	12	60.0	4	21	AAB35866	Peptide used to mo
22	12	60.0	4	21	AAB35867	Peptide used to mo
23	12	60.0	4	21	AAB35874	Peptide used to mo
24	12	60.0	4	21	AAB35875	Peptide used to mo
25	12	60.0	4	21	AAY66960	T cell antigen rec
26	12	60.0	4	22	AAE07173	Mini C-peptide to
27	12	60.0	4	22	AAB91662	Opioid peptide SEQ
28	11	55.0	3	21	AAY66971	T cell antigen rec
29	11	55.0	3	22	AAB92359	Miscellaneous pept
30	11	55.0	4	2	AAP10628	Analgesic tetrapep
31	11	55.0	4	5	AAP40354	Sequence of hydrol
32	11	55.0	4	5	AAP40411	Chromogenic serine
33	11	55.0	4	6	AAP50015	Sequence of a clea
34	11	55.0	4	12	AAR13804	Factor Xa substrat
35	11	55.0	4	12	AAR12867	Chromogenic substr
36	11	55.0	4	12	AAR12870	Chromogenic substr
37	11	55.0	4	12	AAR13803	Factor Xa substrat
38	11	55.0	4	12	AAR13806	Factor Xa substrat
39	11	55.0	4	12	AAR13808	Factor Xa substrat
40	11	55.0	4	13	AAR27101	Sequence of tetrap
41	11	55.0	4	14	AAR32109	Sequence of blood
42	11	55.0	4	14	AAR34871	Endothelin binding
43	11	55.0	4	14	AAR38103	Protease-labile fr
44	11	55.0	4	14	AAR39390	Factor Xa cleavage
45	11	55.0	4	15	AAR54863	Factor Xa cleavage

ALIGNMENTS

RESULT 1
AAG65301
ID AAG65301 standard; protein; 4 AA.
XX
AC AAG65301;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 heavy chain CDR3 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 25; Page 37; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain CDR3 fragment.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEGA 4
||||
Db 1 kega 4

RESULT 2
AAR13812
ID AAR13812 standard; Protein; 4 AA.
XX
AC AAR13812;
XX
DT 07-NOV-1991 (firs entry)
XX
DE Factor Xa substrate peptide (10).
XX
KW Assay; factor Xa; substrate; affinity.
XX
OS Synthetic.
XX
FT Key Location/Qualifiers
FT Modified-site 1
FT /note= "ethyl-D-lysine(carbobenzoxy)"
FT Modified-site 4
FT /note= "L-Arg-HCl"
XX
PN WO9112338-A.
XX
PD 22-AUG-1991.
XX
PF 31-DEC-1990; 90WO-FR00974.
XX
PR 19-FEB-1990; 90FR-0001965.
XX
PA (SERB-) SERBIO.
XX
PI Quentin G, Martinoli JL;
XX
DR WPI; 1991-267149/36.
XX
PT New labelled tri: or tetra:peptide derivs. - substrates for
PT factor Xa assay, with better affinity, selectivity or water
PT solubility
XX
PS Example 91; Page 25; 46pp; French.
XX
CC The peptides represented in AAR13803-12 are examples of a generic
CC formula. They are substrates for assaying factor Xa (an enzyme
CC involved in haemostasis). Compared with known substrates they have
CC better affinity, selectivity and/or water solubility.
XX
SQ Sequence 4 AA;

Query Match 80.0%; Score 16; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEG 3
|||
Db 1 keg 3

RESULT 3
AAY20704
ID AAY20704 standard; Protein; 4 AA.
XX
AC AAY20704;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human neurofilament-M wild type protein fragment 46.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75759.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure; Figure 8; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method

CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
SQ Sequence 4 AA;

Query Match 80.0%; Score 16; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEG 3
||
Db 1 keg 3

RESULT 4
AAW81781
ID AAW81781 standard; Protein; 4 AA.
XX
AC AAW81781;
XX
DT 23-FEB-1999 (first entry)
XX
DE Human HE4 epitope peptide #1.
XX
KW HE4; epididymis-specific; diagnosis; male infertility; treatment;
KW sterility; immunosterilisation.
XX
OS Homo sapiens.
XX
PN EP878544-A1.
XX
PD 18-NOV-1998.
XX
PF 29-JAN-1991; 91EP-0250021.
XX
PR 30-NOV-1990; 90DE-4038189.
PR 01-FEB-1990; 90DE-4002981.
XX
PA (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.
XX
PI Ivell R, Kirchhoff C;
XX
DR WPI; 1998-585748/50.
XX
PT DNA encoding human epididymis polypeptides - useful for, e.g.
PT diagnosis of male infertility
XX
PS Example 9; Page 19; 29pp; German.
XX
CC This sequence represents a novel human epididymis-specific protein, HE4
CC epitope fragment. This protein may be used for cloning and for expression
CC of human epididymis-specific polypeptides in prokaryotic or eukaryotic
CC host cells. Such proteins and antibodies generated from them may be used
CC for diagnosis of e.g. male infertility. The polypeptides and antibodies
CC may also be used for treatment of male infertility and for
CC immunosterilisation of mammals.
XX
SQ Sequence 4 AA;

Query Match 80.0%; Score 16; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEG 3
||
Db 2 keg 4

RESULT 5
AAB62145
ID AAB62145 standard; peptide; 4 AA.
XX
AC AAB62145;
XX
DT 29-MAY-2001 (first entry)
XX
DE P. falciparum FCR3.varCSA protein fragment.
XX
KW FCR3.varCSA protein; chondroitin sulfate A; CSA; var gene; PFEMP1;
KW erythrocyte membrane protein 1; parasitized red blood cell; PRBC;
KW malaria; protozoacide.
XX
OS Plasmodium falciparum.
XX
PN WO200116326-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US24195.
XX
PR 01-SEP-1999; 99US-0152023.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Scherf A, Miller LH, Gamain B, Baruch DI, Buffet P, Scheidig C;
PI Gysin J, Pouvelle B, Fujii N, Smith J;
XX
DR WPI; 2001-235109/24.
XX
PT Novel FCR3.varCSA protein, useful for modulating parasitized red blood
PT cell binding, sequestration and onset of maternal malaria -
XX
PS Disclosure; Page 21; 78pp; English.
XX
CC The invention relates to a P. falciparum FCR3.varCSA protein, that is
CC capable of binding to chondroitin sulfate A (CSA). The var gene and the
CC corresponding P.falciparum erythrocyte membrane protein 1 (PFEMP1)
CC modulate adhesion of parasitized red blood cell (PRBC) to CSA. The
CC protein and the encoding gene are useful for treating and preventing
CC maternal malaria in a patient identified at a risk for contracting
CC maternal malaria or in a patient afflicted with maternal malaria. The
CC present sequence represents a fragment of the P. falciparum FCR3.varCSA
CC protein.
XX
SQ Sequence 4 AA;

Query Match 80.0%; Score 16; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEG 3
||
Db 1 keg 3

RESULT 6
AAY90390
ID AAY90390 standard; peptide; 4 AA.
XX
AC AAY90390;
XX
DT 15-JAN-2001 (first entry)
XX
DE Tumour necrosis factor inhibitor peptide #15.

XX
KW Tumour necrosis factor; inhibitor; TNF-alpha; TNF p55 receptor; cachexia;
KW TNF p75 receptor; sepsis syndrome; circulatory collapse; infection;
KW immune disorder; autoimmune disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; alcohol-induced hepatitis; inflammatory disorder;
KW sarcoidosis; Crohn's disease; vascular inflammatory disease; therapy;
KW disseminated intravascular coagulation; graft-versus-host disease;
KW Rawasaki's disease; malignant disorder; TNF-alpha-secreting tumour.
XX
OS Synthetic.
XX
PN US6107273-A.
XX
PD 22-AUG-2000.
XX
PF 24-JAN-1995; 95US-0377781.
XX
PR 24-JAN-1995; 95US-0377781.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Jameson BA, Noe M;
XX
DR WPI; 2000-571331/53.
XX
PT Novel tumor necrosis factor inhibitors for treating disorders mediated
PT by tumor necrosis factor alpha activity e.g. autoimmune disorders,
PT pathogenic infections, malignant tumors and cachexia -
XX
PS Disclosure; Column 8; 17pp; English.
XX
CC This sequence represents a fragment of a tumour necrosis factor inhibitor
CC of the invention. The inhibitors are antagonists of tumour necrosis
CC factor-alpha (TNF-alpha), comprising less than 15 amino acids, having
CC restricted conformation and capable of binding to TNF p55 and/or TNF p75
CC receptor. The inhibitors are useful for treating a disease or condition
CC mediated by TNF-alpha such as sepsis syndrome, cachexia, circulatory
CC collapse and shock resulting from acute or chronic bacterial infection;
CC acute and chronic parasitic or infectious processes, including bacterial,
CC viral and fungal infections; acute and chronic immune and autoimmune
CC disorder, such as systemic lupus erythematosus and rheumatoid arthritis,
CC alcohol-induced hepatitis; chronic inflammatory disorder such as
CC sarcoidosis and Crohn's disease; vascular inflammatory disorder such as
CC disseminated intravascular coagulation, graft-versus-host disease,
CC Rawasaki's disease, and malignant disorders involving TNF-alpha-secreting
CC tumours.
XX
SQ Sequence 4 AA;

Query Match 75.0%; Score 15; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGA 4
:||
Db 1 ega 3

RESULT 7
AAW56198
ID AAW56198 standard; peptide; 3 AA.
XX
AC AAW56198;
XX
DT 20-JUL-1998 (first entry)
XX
DE Anti-inflammatory tripeptide.
XX
KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX
OS Synthetic.
XX
PN WO9809985-A2.
XX
PD 12-MAR-1998.
XX
PF 03-SEP-1997; 97WO-IL00295.
XX
PR 28-MAY-1997; 97US-0864301.
PR 03-SEP-1996; 96US-0025376.
PR 20-NOV-1996; 96US-0753141.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX
DR WPI; 1998-193550/17.
XX
PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX
PS Claim 5; Page 34; 42pp; English.
XX
CC AAW56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be
CC used to inhibit unwanted immune reaction and inflammation.
XX
SQ Sequence 3 AA;

Query Match 65.0%; Score 13; DB 19; Length 3;
Best Local Similarity 66.7%; Pred. No. 6.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEG 3
:||
Db 1 reg 3

RESULT 8
AAW05773
ID AAW05773 standard; peptide; 4 AA.
XX
AC AAW05773;
XX
DT 28-JUL-1997 (first entry)
XX
DE Presenilin-1-1 residues 109-112.
XX
KW Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; mutein.
XX
OS Homo sapiens.
XX
PN WO9634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA00263.

```
XX
PR   31-JUL-1995;   95US-0509359.
PR   28-APR-1995;   95US-0431048.
PR   28-JUN-1995;   95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 71; Page -; 178pp; English.
XX
CC   AAW05768-W05788 represent antigenic fragments of the human
CC   presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734
CC   represents a different wild type form of presenilin-1 that results from
CC   alternate splicing of the genomic DNA sequence. The presenilins are a
CC   family of highly conserved integral membrane proteins with a common
CC   structural motif, common alternate splicing patterns, and common
CC   mutational hot spot regions. Mutations in PS genes are implicated in
CC   familial Alzheimer's disease (AD) and possibly other diseases such as
CC   cerebral haemorrhage, schizophrenia, depression etc., so detection of
CC   mutations in the DNA encoding the wild type sequences can be used for
CC   diagnosis of these diseases. The wild type proteins, or vectors that
CC   express them or containing antisense sequences, antibodies selective for
CC   these mutant forms of the proteins and modulators of PS gene expression
CC   are potentially useful for treatment of AD etc. Transgenic animals are
CC   useful as models for drug screening. The antibodies can also be used e.g.
CC   for affinity purification and in immunoassays.
XX
SQ   Sequence   4 AA;


  Query Match             65.0%;  Score 13;  DB 17;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEG 3
           |:|
Db       1 kdg 3


RESULT   9
AAP40366
ID   AAP40366 standard; peptide; 4 AA.
XX
AC   AAP40366;
XX
DT   11-FEB-1992  (first entry)
XX
DE   Sequence of inhibitor of pancreatic and leucocytic elastase.
XX
KW   Pancreatitis therapy; emphysema; arthritis.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /label= N-alpha-ac-Asp
XX
PN   BE897844-A.
XX
PD   16-JAN-1984.
XX
PF   27-SEP-1983;   83BE-0897844.
XX
PR   01-OCT-1982;   82CS-0007013.
XX
PA   (SPOF ) SPOFA SPOJENE PODN.
PA   (KASA/) KASAFIREK E.
XX
PI   Kasafirek E,  Fric P,  Slaby J,  Roubalova A;
XX
DR   WPI; 1984-037109/07.
XX
PT   Tri:peptide and tetra:peptide elastase inhibitors - used to treat
PT   acute pancreatitis, chronic obstructive pulmonary disease e.g.
PT   emphysema and some forms of arthritis
XX
PS   Claim 9; Page 13; 19pp; French.
XX
CC   The peptides of the invention may be used to treat acute
CC   pancreatitis, chronic obstructive pulmonary disease (pulmonary
CC   emphysema) and certain forms of arthritis.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 5;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EGA 4
           :||
Db       1 dga 3


RESULT   10
AAR23938
ID   AAR23938 standard; Protein; 4 AA.
XX
AC   AAR23938;
XX
DT   15-NOV-1992  (first entry)
XX
DE   Lactoferrin-introduced peptide (8).
XX
KW   Human lactoferrin; LF; transformation; ss.
XX
OS   Synthetic.
XX
PN   JP04108390-A.
XX
PD   09-APR-1992.
XX
PF   29-AUG-1990;   90JP-0227619.
XX
PR   29-AUG-1990;   90JP-0227619.
XX
PA   (SNOW ) SNOW BRAND MILK PRO.
XX
DR   WPI; 1992-171655/21.
XX
PT   Introduction of foreign genes into animal cells - using a
PT   complex comprising the gene with lactoferrin.
XX
PS   Disclosure; Page 5; 10pp; Japanese.
XX
CC   The sequences given in AAR23931 - AAR23938 are synthetic peptides which
CC   were introduced into human lactoferrin (LF) by introducing the DNA
CC   encoding the peptide into the human LF gene and then incubating the
CC   mixture.  The introduction of the peptide caused increased
CC   transformation rates compared to unmodified LF and this method could
CC   be used to introduce an exogenous gene into an animal cell with no
CC   stress.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 13;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 KEG 3
```

```
          |:|
Db      2 kkg 4


RESULT  11
AAR75498
ID   AAR75498 standard; Peptide; 4 AA.
XX
AC   AAR75498;
XX
DT   13-NOV-1995  (first entry)
XX
DE   C5a receptor-antagonist core tetrapeptide.
XX
KW   C5a; C5a receptor-antagonist; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO9516033-A.
XX
PD   15-JUN-1995.
XX
PF   16-NOV-1994;   94WO-IB00359.
XX
PR   06-DEC-1993;   93US-0162591.
XX
PA   (CIBA ) CIBA GEIGY AG.
XX
PI   Boyar WC,  Galakatos NG,  Peppard JV,  Van Oostrum J;
XX
DR   WPI; 1995-224319/29.
XX
PT   C5a receptor antagonists having no agonist activity - are used in
PT   compsns. to treat C5a-mediated diseases and inflammatory conditions
XX
PS   Disclosure; Page 36; 65pp; English.
XX
CC   Polypeptide receptor antagonists to C5a contain an essential core
CC   tetrapeptide (AAR75498 or AAR75499) or core tripeptide (DGA) which
CC   displays C5a blocking activity.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 16;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 EGA 4
          :||
Db      2 dga 4


RESULT  12
AAR75499
ID   AAR75499 standard; Peptide; 4 AA.
XX
AC   AAR75499;
XX
DT   13-NOV-1995  (first entry)
XX
DE   C5a receptor-antagonist core tetrapeptide.
XX
KW   C5a; C5a receptor-antagonist; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO9516033-A.
XX
PD   15-JUN-1995.
XX
PF   16-NOV-1994;   94WO-IB00359.
XX
PR   06-DEC-1993;   93US-0162591.
XX
PA   (CIBA ) CIBA GEIGY AG.
XX
PI   Boyar WC,  Galakatos NG,  Peppard JV,  Van Oostrum J;
XX
DR   WPI; 1995-224319/29.
XX
PT   C5a receptor antagonists having no agonist activity - are used in
PT   compsns. to treat C5a-mediated diseases and inflammatory conditions
XX
PS   Disclosure; Page 36; 65pp; English.
XX
CC   Polypeptide receptor antagonists to C5a contain an essential core
CC   tetrapeptide (AAR75498 or AAR75499) or core tripeptide (DGA) which
CC   displays C5a blocking activity.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 16;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 EGA 4
          :||
Db      1 dga 3


RESULT  13
AAW27455
ID   AAW27455 standard; peptide; 4 AA.
XX
AC   AAW27455;
XX
DT   21-APR-1998  (first entry)
XX
DE   Beta-endorphin C-terminal fragment 1.
XX
KW   Beta-endorphin; diabetes mellitus; glucose uptake; insulin; muscle.
XX
OS   Class Mammalia.
XX
PN   WO9735608-A1.
XX
PD   02-OCT-1997.
XX
PF   21-MAR-1997;   97WO-GB00795.
XX
PR   22-MAR-1996;   96GB-0006076.
XX
PA   (UNBI ) UNIV BIRMINGHAM.
XX
PI   Smith ME;
XX
DR   WPI; 1997-489388/45.
XX
PT   Use of peptide including active carboxy-terminal fragment of
PT   beta-endorphin  - to treat diabetes mellitus or increase uptake of
PT   blood glucose in muscle
XX
PS   Claim 8; Page 11; 18pp; English.
XX
CC   This peptide is an active carboxy-terminal fragment derived from
CC   beta-endorphin.  The peptide or an active analogue can be used in the
CC   manufacture of a medicament for the treatment of diabetes mellitus, by
CC   increasing uptake of blood glucose in muscle.  The peptide does not
CC   include the opioid amino-terminal region of beta-endorphin, and enhances
CC   uptake of glucose into muscle by a non-insulin dependent route.
XX
SQ   Sequence   4 AA;
```

```
  Query Match             60.0%;  Score 12;  DB 18;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 KEG 3
          |:|
Db      1 kkg 3


RESULT  14
AAW27456
ID   AAW27456 standard; peptide; 4 AA.
XX
AC   AAW27456;
XX
DT   21-APR-1998  (first entry)
XX
DE   Beta-endorphin C-terminal fragment 2.
XX
KW   Beta-endorphin; diabetes mellitus; glucose uptake; insulin; muscle.
XX
OS   Class Mammalia.
XX
PN   WO9735608-A1.
XX
PD   02-OCT-1997.
XX
PF   21-MAR-1997;   97WO-GB00795.
XX
PR   22-MAR-1996;   96GB-0006076.
XX
PA   (UNBI ) UNIV BIRMINGHAM.
XX
PI   Smith ME;
XX
DR   WPI; 1997-489388/45.
XX
PT   Use of peptide including active carboxy-terminal fragment of
PT   beta-endorphin  - to treat diabetes mellitus or increase uptake of
PT   blood glucose in muscle
XX
PS   Claim 8; Page 11; 18pp; English.
XX
CC   This peptide is an active carboxy-terminal fragment derived from
CC   beta-endorphin.  The peptide or an active analogue can be used in the
CC   manufacture of a medicament for the treatment of diabetes mellitus, by
CC   increasing uptake of blood glucose in muscle.  The peptide does not
CC   include the opioid amino-terminal region of beta-endorphin, and enhances
CC   uptake of glucose into muscle by a non-insulin dependent route.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 18;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 KEG 3
          |:|
Db      1 kkg 3


RESULT  15
AAW27457
ID   AAW27457 standard; peptide; 4 AA.
XX
AC   AAW27457;
XX
DT   21-APR-1998  (first entry)
XX
DE   Beta-endorphin C-terminal fragment 3.
XX
KW   Beta-endorphin; diabetes mellitus; glucose uptake; insulin; muscle.
XX
OS   Class Mammalia.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal acetyl"
FT   Misc-difference 2
FT                   /note= "D-form residue"
FT   Modified-site   3
FT                   /label= MeGly
FT                   /note= "Sarcosine"
XX
PN   WO9735608-A1.
XX
PD   02-OCT-1997.
XX
PF   21-MAR-1997;   97WO-GB00795.
XX
PR   22-MAR-1996;   96GB-0006076.
XX
PA   (UNBI ) UNIV BIRMINGHAM.
XX
PI   Smith ME;
XX
DR   WPI; 1997-489388/45.
XX
PT   Use of peptide including active carboxy-terminal fragment of
PT   beta-endorphin  - to treat diabetes mellitus or increase uptake of
PT   blood glucose in muscle
XX
PS   Claim 12; Page 11; 18pp; English.
XX
CC   This peptide is an active carboxy-terminal fragment derived from
CC   beta-endorphin.  The peptide or an active analogue can be used in the
CC   manufacture of a medicament for the treatment of diabetes mellitus, by
CC   increasing uptake of blood glucose in muscle.  Although a known
CC   peptide, this modified form is more stable and can be administered
CC   orally, as compaared to the unmodified form which is given
CC   intravenously, subcutaneously or intramuscularly. The peptide does not
CC   include the opioid amino-terminal region of beta-endorphin, and enhances
CC   uptake of glucose into muscle by a non-insulin dependent route.
XX
SQ   Sequence   4 AA;


  Query Match             60.0%;  Score 12;  DB 18;  Length 4;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 KEG 3
          |:|
Db      1 kkg 3


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GenCore version 4.5

OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 52936

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Maximum DB seq length: 7

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Listing first 45 summaries

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18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	7	21	AAY95196	Anti-platelet glyc
2	39	100.0	7	21	AAY95217	Anti-platelet glyc
3	39	100.0	7	22	AAG65303	Anti-IL-18 antibod
4	34	87.2	7	22	AAG63624	Complementarity de
5	29	74.4	7	20	AAY06691	Ab1 variable light
6	24	61.5	7	19	AAW39828	Light chain CDR3 o
7	24	61.5	7	19	AAW39831	Light chain CDR2 o
8	24	61.5	7	21	AAB40010	Anti-hIL12 antibod
9	23	59.0	7	20	AAW90303	Human anti-GPIIb/I
10	23	59.0	7	21	AAB30605	Anti-IgE antibody
11	23	59.0	7	21	AAB39504	Anti-hIL-12 antibo
12	23	59.0	7	21	AAB40001	Anti-hIL12 antibod
13	23	59.0	7	21	AAB40012	Anti-hIL12 antibod
14	23	59.0	7	21	AAB40013	Anti-hIL12 antibod
15	23	59.0	7	21	AAB40014	Anti-hIL12 antibod
16	23	59.0	7	21	AAW90831	Rat nervous system
17	23	59.0	7	21	AAY79089	Anti-factor IX/IXa
18	22	56.4	7	15	AAR54140	CHA255 light chain
19	22	56.4	7	16	AAR73900	Haemophilus influe
20	22	56.4	7	20	AAW90304	Human anti-GPIIb/I
21	22	56.4	7	21	AAB52206	Human anti-HBs ant
22	22	56.4	7	21	AAY95207	Anti-platelet glyc
23	22	56.4	7	22	AAB61285	Anti-TANGO 268 scF
24	22	56.4	7	22	AAB61297	Anti-TANGO 268 scF
25	22	56.4	7	22	AAB66404	Anti-TANGO 268 scF
26	21	53.8	7	21	AAB40011	Anti-hIL12 antibod
27	21	53.8	7	21	AAB40015	Anti-hIL12 antibod
28	21	53.8	7	21	AAB40017	Anti-hIL12 antibod
29	20	51.3	7	21	AAB40016	Anti-hIL12 antibod
30	20	51.3	7	22	AAG62817	Amino acid sequenc
31	20	51.3	7	22	AAB80721	Human glandular ka
32	20	51.3	7	22	AAB29546	Adhesion-modulator
33	19	48.7	5	16	AAR77331	Human apolipoprote
34	19	48.7	5	19	AAY20765	Human neurofilamen
35	19	48.7	5	21	AAY63117	LI-cadherin cell a
36	19	48.7	5	21	AAY63147	LI-cadherin cell a
37	19	48.7	6	14	AAR33819	Selectin binding i
38	19	48.7	6	17	AAR96652	Kininogen-derived
39	19	48.7	6	21	AAB15429	Cell differentiati
40	19	48.7	6	21	AAB01542	Plasmin substrate
41	19	48.7	6	21	AAY63118	LI-cadherin cell a
42	19	48.7	6	21	AAY63148	LI-cadherin cell a
43	19	48.7	6	22	AAG65314	Anti-IL-18 antibod
44	19	48.7	7	11	AAR06760	Tumour necrosis fa
45	19	48.7	7	14	AAR33815	Selectin binding i

ALIGNMENTS

RESULT 1
AAY95196
ID AAY95196 standard; Peptide; 7 AA.
XX
AC AAY95196;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-1 VL CDR2.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-1;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -

XX
PS Claim 20; Fig 5; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 2 (CDR2) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-1 (see AAY95198), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 39; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 1 gknnrps 7

RESULT 2
AAY95217
ID AAY95217 standard; Peptide; 7 AA.
XX
AC AAY95217;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-3 VL CDR2.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-3;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR2;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Claim 20; Fig 7; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 2 (CDR2) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-3 (see AAY95219), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 39; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 1 gknnrps 7

RESULT 3
AAG65303
ID AAG65303 standard; protein; 7 AA.
XX
AC AAG65303;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR2 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 27; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain CDR2 fragment.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 39; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
|||||||
Db 1 gknnrps 7

RESULT 4
AAG63624
ID AAG63624 standard; peptide; 7 AA.
XX
AC AAG63624;
XX
DT 29-OCT-2001 (first entry)
XX
DE Complementarity determining region (CDR) 2 of ScFv1-4 H chain.
XX
KW Complementarity determining region; CDR; single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW envelope glycoprotein.
XX
OS Homo sapiens.
XX
PN WO200158459-A1.
XX
PD 16-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-JP00967.
XX
PR 14-FEB-2000; 2000JP-0034906.
XX
PA (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR WPI; 2001-496986/54.
XX
PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope
PT glycoprotein or CD81 -
XX
PS Claim 24; Page 75; 138pp; Japanese.
XX
CC The present sequence represents a complementarity determining region
CC (CDR) of a single chain (ScFv) antibody of the invention. The
CC specification describes a substance can inhibit the binding between
CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC with expression of CD81, or CD81. This substance is especially an
CC antibody with affinity towards HCV E2/NS1 protein, containing amino
CC acid sequences based on the CDR1, CDR2 and CDR3 of the H and L chain
CC variable regions. The antibody inhibits the viral envelope glycoprotein.
CC It is also a CD81 inhibitor. The antibodies and drugs are used for
CC treatment and/or prevention of hepatitis C, or for diagnosis of
CC hepatitis C.
XX
SQ Sequence 7 AA;

Query Match 87.2%; Score 34; DB 22; Length 7;
Best Local Similarity 85.7%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| |||||
Db 1 gnnnrps 7

RESULT 5
AAY06691
ID AAY06691 standard; Protein; 7 AA.
XX
AC AAY06691;
XX
DT 17-JUN-1999 (first entry)
XX
DE Ab1 variable light (VL) chain CDR2.
XX
KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour;, MuSK; CDR;
KW neuromuscular; muscular dystrophy; complementarity determining region;
KW variable heavy chain; variable light chain; VH; VL.
XX
OS Homo sapiens.
XX
PN WO9910494-A2.
XX
PD 04-MAR-1999.
XX
PF 21-AUG-1998; 98WO-US17364.
XX
PR 25-AUG-1997; 97US-0918148.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX
DR WPI; 1999-204666/17.
DR N-PSDB; AAX32391.
XX
PT New thrombopoietin receptor agonist antibodies - useful for
PT treating immunological or hematological disorders
XX
PS Claim 10; Page 75; 86pp; English.
XX
CC The invention relates to an agonist antibody (Ab) which binds to a
CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
CC be used in the same way and for the same indications as thrombopoietin
CC (TPO). They can stimulate proliferation, differentiation or growth of
CC megakaryocytes. They may also be able to stimulate megakaryocytes to
CC increase platelet production. They can be used for treating
CC immunological or hematopoietic disorders, especially thrombocytopenia.
CC Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
CC following chemotherapy or bone marrow transplant) may be effectively
CC treated with the antibody compounds as well as disorders such as
CC disseminated intravascular coagulation (DIC), immune thrombocytopenia
CC (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
CC congenital thrombocytopenia, thrombotic thrombocytopenia and
CC myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
CC treatment of solid tumours or leukaemia, myeloablative chemotherapy for
CC autologous or allogeneic bone marrow transplant, myelodysplasia,
CC idiopathic aplastic anemia, congenital thrombocytopenia, and immune
CC thrombocytopenia. The antibodies which bind to the MuSK receptor can be
CC used for improving neuromuscular function in a patient, e.g. in muscular
CC dystrophy. The products can also be used for detection and diagnosis. The

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CC   antibodies have a longer half-life than the natural ligand for the TPO-R.
CC   Sequences AAY06687-Y06712 represent CDR1, CDR2, and CDR3 regions of
CC   variable heavy (VH) chains and variable light (VL) chains of antibodies
CC   Ab1 to Ab6.
XX
SQ   Sequence   7 AA;


  Query Match             74.4%;  Score 29;  DB 20;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GKNNRPS 7
          | :||||
Db      1 gnsnrps 7


RESULT   6
AAW39828
ID   AAW39828 standard; peptide; 7 AA.
XX
AC   AAW39828;
XX
DT   16-JUN-1998  (first entry)
XX
DE   Light chain CDR3 of catalytic antibody 9A3.
XX
KW   Variable domain; lambda light chain; catalytic antibody; degradation;
KW   cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW   phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW   overdose; addiction.
XX
OS   Mus sp.
XX
PN   WO9749800-A1.
XX
PD   31-DEC-1997.
XX
PF   25-JUN-1997;   97WO-US10965.
XX
PR   25-JUN-1996;   96US-0672345.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Landry DW;
XX
DR   WPI; 1998-077166/07.
XX
PT   New catalytic antibodies able to decompose cocaine, single-chain
PT   analogues - used to treat cocaine overdose and addiction, required
PT   in far smaller doses than antibodies that antagonise cocaine by
PT   simply binding
XX
PS   Claim 6; Page 84; 147pp; English.
XX
CC   AAW39827-29 represent the sequences of the light chain complementarity
CC   determining regions (CDRs) of the catalytic antibody 9A3, which is able
CC   to degrade cocaine. A series of cocaine transition state analogues
CC   (TSAs) were prepared and used to immunise mice for production of
CC   hybridomas. Catalytic antibodies were identified by their capacity to
CC   release 3H-benzoic acid from 3H-phenyl cocaine. The 9A3 antibody was
CC   identified using TSA1, which is an immunogenic conjugate of a phosphate
CC   monoester transition state analogue. Antibody 9A3 has a per minute Kcat
CC   of 0.015. The antibodies reduce the concentration of cocaine in a
CC   subject, and are used particularly for the treatment of an overdose. They
CC   are also used for treating addiction (by reducing the in vivo
CC   concentration that can be achieved).
XX
SQ   Sequence   7 AA;


  Query Match             61.5%;  Score 24;  DB 19;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 NNRP 6
          ||||
Db      3 nnrp 6


RESULT   7
AAW39831
ID   AAW39831 standard; peptide; 7 AA.
XX
AC   AAW39831;
XX
DT   16-JUN-1998  (first entry)
XX
DE   Light chain CDR2 of catalytic antibody 19G8.
XX
KW   Variable domain; lambda light chain; catalytic antibody; degradation;
KW   cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW   phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW   overdose; addiction.
XX
OS   Mus sp.
XX
PN   WO9749800-A1.
XX
PD   31-DEC-1997.
XX
PF   25-JUN-1997;   97WO-US10965.
XX
PR   25-JUN-1996;   96US-0672345.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Landry DW;
XX
DR   WPI; 1998-077166/07.
XX
PT   New catalytic antibodies able to decompose cocaine, single-chain
PT   analogues - used to treat cocaine overdose and addiction, required
PT   in far smaller doses than antibodies that antagonise cocaine by
PT   simply binding
XX
PS   Claim 4; Page 85; 147pp; English.
XX
CC   AAW39830-32 represent the sequences of the light chain complementarity
CC   determining regions (CDRs) of the catalytic antibody 19G8, which is able
CC   to degrade cocaine. A series of cocaine transition state analogues
CC   (TSAs) were prepared and used to immunise mice for production of
CC   hybridomas. Catalytic antibodies were identified by their capacity to
CC   release 3H-benzoic acid from 3H-phenyl cocaine. The 19G8 antibody was
CC   identified using TSA1, which is an immunogenic conjugate of a phosphate
CC   monoester transition state analogue. Antibody 19G8 has a per minute Kcat
CC   of 0.091. The antibodies reduce the concentration of cocaine in a
CC   subject, and are used particularly for the treatment of an overdose. They
CC   are also used for treating addiction (by reducing the in vivo
CC   concentration that can be achieved).
XX
SQ   Sequence   7 AA;


  Query Match             61.5%;  Score 24;  DB 19;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 NNRP 6
          ||||
Db      3 nnrp 6


RESULT   8
AAB40010
ID   AAB40010 standard; Peptide; 7 AA.
```

XX
AC AAB40010;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 526.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2G; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 61.5%; Score 24; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| ::|||
Db 1 gndsrps 7

RESULT 9
AAW90303
ID AAW90303 standard; Protein; 7 AA.
XX
AC AAW90303;
XX
DT 07-SEP-1999 (first entry)
XX
DE Human anti-GPIIb/IIIa auto-antibody light chain protein CDR2 region 1.
XX
KW Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
KW blood platelet membrane protein; predisposition; prevention; treatment;
KW autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombi;
KW thrombocyte; cardiac infarction; pulmonary embolism; light chain.
XX
OS Homo sapiens.
XX
PN WO9855619-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-EP03397.
XX
PR 08-MAY-1998; 98DE-1020663.
PR 06-JUN-1997; 97DE-1023904.
PR 12-DEC-1997; 97DE-1055227.
XX
PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX
PI Berchtold P, Escher RFA;
XX
DR WPI; 1999-105496/09.
XX
PT Nucleic acid encoding human autoantibodies against platelet
PT glycoprotein IIb/IIIa - used for diagnosis, treatment and prevention
PT of autoimmune thrombocytopaenic purpura and for modulation of
PT fibrinogen binding
XX
PS Claim 6a; Page 6; 93pp; German.
XX
CC This invention describes novel nucleic acid fragments that encode human
CC auto-antibodies and anti-idiotypic antibodies against blood platelet
CC membrane protein, GPIIb/IIIa. The products of the invention are used
CC for diagnosis (including monitoring and determining predisposition),
CC prevention and treatment of autoimmune thrombocytopaenic purpura (AITP)
CC and also for modulating binding of fibrinogen to thrombocytes
CC (particularly to dissolve thrombi and/or prevent their formation, e.g.
CC in cases of cardiac infarction or pulmonary embolism). Unlike murine
CC antibodies, human antibodies (hAb) do not induce adverse side effects
CC and persist for longer in vivo than small peptides. AAW90293-W90337
CC represent antibody fragments used in the method of the invention.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 20; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gshqrps 7

RESULT 10
AAB30605
ID AAB30605 standard; peptide; 7 AA.
XX
AC AAB30605;
XX
DT 19-MAR-2001 (first entry)
XX
DE Anti-IgE antibody light chain complementarity determining region 2.
XX

KW Anti-idiotype antibody; C-epsilon3 region; immunoglobulin E; IgE;
KW anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;
KW rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
KW passive immunisation.
XX
OS Homo sapiens.
XX
PN WO200063252-A1.
XX
PD 26-OCT-2000.
XX
PF 12-APR-2000; 2000WO-EP03288.
XX
PR 14-APR-1999; 99GB-0008533.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Kricek F, Stadler B, Vogel M;
XX
[redacted] WPI; 2000-687161/67.
XX
PT Novel anti-idiotypic antibody against antibodies which inhibit binding
PT of immunoglobulin E to its high affinity receptor, useful in vaccines
PT for treating diseases such as allergy, rhinitis, atopic dermatitis -
XX
PS Claim 5; Page 67; 73pp; English.
XX
CC AAB30595-B30606 represent complementarity determining regions (CDRs)
CC from human anti-idiotype antibodies that interfere with the binding of
CC the C-epsilon3 region of immunoglobulin (Ig)E to the high affinity
CC receptor for IgE, i.e. and anti-IgE antibody. Such an antibody is
CC referred to as a mimobody. The anti-IgE antibody fragment is used as a
CC vaccine, and as a pharmaceutical for treating IgE-mediated diseases such
CC as allergy, in particular asthma, atopic dermatitis, rhinitis, chronic
CC urticaria and food allergies. It is also used to treat IgE-mediated
CC diseases. It is also used for raising polyclonal or monoclonal
CC antibodies. The polyclonal or monoclonal antibodies obtained are useful
CC for treating IgE-mediated diseases by passive immunisation.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NNRPS 7
:||||
Db 3 snrps 7

RESULT 11
AAB39504
ID AAB39504 standard; Protein; 7 AA.
XX
AC AAB39504;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL-12 antibody light chain CDR2 amino acid sequence SEQ ID 20.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 24; Page 232; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gndqrps 7

RESULT 12
AAB40001
ID AAB40001 standard; Peptide; 7 AA.
XX
AC AAB40001;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 517.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.

XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2G; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gndqrps 7

RESULT 13
AAB40012
ID AAB40012 standard; Peptide; 7 AA.
XX
AC AAB40012;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 528.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.

XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2G; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gndrrps 7

RESULT 14
AAB40013
ID AAB40013 standard; Peptide; 7 AA.
XX
AC AAB40013;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 529.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.

XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2G; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gndqrps 7

RESULT 15
AAB40014
ID AAB40014 standard; Peptide; 7 AA.
XX
AC AAB40014;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 530.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2G; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 7 AA;

Query Match 59.0%; Score 23; DB 21; Length 7;
Best Local Similarity 57.1%; Pred. No. 6.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GKNNRPS 7
| : |||
Db 1 gndtrps 7

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Job time: 159 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 12, 2002, 11:11:05 ; Search time 48.93 Seconds
(without alignments)
24.971 Million cell updates/sec

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Perfect score: 55
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 147623

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Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	11	22	AAG65304	Anti-IL-18 antibod
2	42	76.4	11	22	AAG62970	Complementarity de
3	42	76.4	11	22	AAG62974	Complementarity de
4	42	76.4	11	22	AAG62976	Complementarity de
5	42	76.4	11	22	AAG62980	Complementarity de
6	42	76.4	11	22	AAG62984	Complementarity de
7	39	70.9	11	22	AAG62972	Complementarity de
8	39	70.9	11	22	AAG62982	Complementarity de
9	39	70.9	11	22	AAG62998	Complementarity de
10	35	63.6	9	22	AAU02694	CDR region of anti
11	34	61.8	9	21	AAY95197	Anti-platelet glyc
12	34	61.8	9	21	AAY95218	Anti-platelet glyc
13	32	58.2	10	17	AAR88543	Varicella zoster g
14	32	58.2	11	22	AAU08356	Antibody light cha
15	30	54.5	11	19	AAW62282	Synthetic immunogl
16	28	50.9	10	22	AAG97060	Human complementar
17	26	47.3	6	17	AAR88549	Varicella zoster g
18	26	47.3	11	14	AAR30164	MAb 1-3-1 variable
19	25	45.5	10	22	AAG95162	Human complementar
20	25	45.5	10	22	AAG86891	Saccharomyces cere
21	24	43.6	9	20	AAY47834	Immunogenic peptid
22	24	43.6	9	22	AAB75900	Hepatitis B virus
23	24	43.6	9	22	AAB75901	Hepatitis B virus
24	24	43.6	10	16	AAW21482	Schistosoma elasta
25	24	43.6	10	22	AAG96424	Human complementar
26	24	43.6	10	22	AAG96430	Human complementar
27	24	43.6	10	22	AAG96432	Human complementar
28	24	43.6	10	22	AAG97032	Human complementar
29	24	43.6	10	22	AAG97034	Human complementar
30	24	43.6	10	22	AAG83494	Arabidopsis thalia
31	24	43.6	10	22	AAG85139	Saccharomyces cere
32	24	43.6	10	22	AAG87059	Saccharomyces cere
33	24	43.6	10	22	AAG87964	Saccharomyces cere
34	24	43.6	10	22	AAG87965	Saccharomyces cere
35	24	43.6	10	22	AAG88169	Saccharomyces cere
36	23	41.8	5	18	AAW28455	PECAM-1 cyclic inh
37	23	41.8	5	18	AAW28436	PECAM-1 inhibitor
38	23	41.8	5	18	AAW28439	PECAM-1 inhibitor
39	23	41.8	5	18	AAW28379	PECAM-1 inhibitor
40	23	41.8	6	18	AAW28454	PECAM-1 cyclic inh
41	23	41.8	6	18	AAW28428	PECAM-1 inhibitor
42	23	41.8	6	18	AAW28434	PECAM-1 inhibitor
43	23	41.8	8	13	AAR25461	wohl-8. Synthetic
44	23	41.8	8	13	AAR26212	Sequence of angiog
45	23	41.8	8	16	AAR61400	PF4-related octape

ALIGNMENTS

RESULT 1
AAG65304
ID AAG65304 standard; protein; 11 AA.
XX
AC AAG65304;
XX
DT 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody 2E1 light chain CDR3 fragment.
XX
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
OS Homo sapiens.
XX
PN WO200158956-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04170.
XX
PR 10-FEB-2000; 2000US-0181608.
XX
PA (BADI) BASF AG.
XX
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
XX
DR WPI; 2001-550020/61.
XX
PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -
XX
PS Claim 27; Page 38; 91pp; English.
XX
CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain CDR3 fragment.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 55; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSRDSSGIHVV 11
||||||||||
Db 1 gsrdssgihvv 11

RESULT 2
AAG62970
ID AAG62970 standard; peptide; 11 AA.
XX
AC AAG62970;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G65.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 3
AAG62974
ID AAG62974 standard; peptide; 11 AA.
XX
AC AAG62974;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G73.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for

CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 4
AAG62976
ID AAG62976 standard; peptide; 11 AA.
XX
AC AAG62976;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G76.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 76.4%; Score 42; DB 22; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| |||
Db 2 srdssgnhvv 11

RESULT 5
AAG62980
ID AAG62980 standard; peptide; 11 AA.
XX
AC AAG62980;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G78.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

```
  Query Match             76.4%;  Score 42;  DB 22;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 0.097;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| |||
Db       2 srdssgnhvv 11


RESULT   6
AAG62984
ID   AAG62984 standard; peptide; 11 AA.
XX
AC   AAG62984;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Complementarity determining region 3 (CDR3) of VL chain of clone G81.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases  -
XX
PS   Claim 1; Page 76; 109pp; English.
XX
CC   AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC   of VL and VH chains of antibodies of the invention. The specification
CC   describes a mixture or panel of 5 different specific binding members,
CC   each comprising an antibody VH and/or VL variable domain and capable,
CC   when displayed on the surface of filamentous bacteriophage particles or
CC   in the case of a specific binding member comprising the D5 VH and/or VL
CC   variable domain when bound to human serum amyloid protein, to pass
CC   through a mammalian blood brain barrier (BBB). The panel is useful for
CC   the selection of specific binding members with a desired property such
CC   as ability to cross BBB, ability to bind endothelial cells or other brain
CC   cell antigen, ability to bind areas of inflammation in the brain or BBB
CC   breakdown or ability to bind intracellular adhesion molecules and to bind
CC   transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC   and treatment of human or animal body, including neurological diseases,
CC   such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC   epilepsy and traumatic brain injury and any diseases involving
CC   inflammation occurring within the brain or central nervous system.
XX
SQ   Sequence   11 AA;


  Query Match             76.4%;  Score 42;  DB 22;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 0.097;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| |||
Db       2 srdssgnhvv 11


RESULT   7
AAG62972
ID   AAG62972 standard; peptide; 11 AA.
XX
AC   AAG62972;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Complementarity determining region 3 (CDR3) of VL chain of clone G67.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases  -
XX
PS   Claim 1; Page 76; 109pp; English.
XX
CC   AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC   of VL and VH chains of antibodies of the invention. The specification
CC   describes a mixture or panel of 5 different specific binding members,
CC   each comprising an antibody VH and/or VL variable domain and capable,
CC   when displayed on the surface of filamentous bacteriophage particles or
CC   in the case of a specific binding member comprising the D5 VH and/or VL
CC   variable domain when bound to human serum amyloid protein, to pass
CC   through a mammalian blood brain barrier (BBB). The panel is useful for
CC   the selection of specific binding members with a desired property such
CC   as ability to cross BBB, ability to bind endothelial cells or other brain
CC   cell antigen, ability to bind areas of inflammation in the brain or BBB
CC   breakdown or ability to bind intracellular adhesion molecules and to bind
CC   transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC   and treatment of human or animal body, including neurological diseases,
CC   such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC   epilepsy and traumatic brain injury and any diseases involving
CC   inflammation occurring within the brain or central nervous system.
XX
SQ   Sequence   11 AA;


  Query Match             70.9%;  Score 39;  DB 22;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 0.37;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SRDSSGIHVV 11
           |||||| ||:
Db       2 srdssgnhvl 11


RESULT   8
AAG62982
```

ID AAG62982 standard; peptide; 11 AA.
XX
AC AAG62982;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G79.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 70.9%; Score 39; DB 22; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| ||:
Db 2 srdssgnhvl 11

RESULT 9
AAG62998
ID AAG62998 standard; peptide; 11 AA.
XX
AC AAG62998;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VL chain of clone G101.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB04501.
XX
PR 13-DEC-1999; 99US-0170599.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such
CC as ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system.
XX
SQ Sequence 11 AA;

Query Match 70.9%; Score 39; DB 22; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| ||:
Db 2 srdssgnhvl 11

RESULT 10
AAU02694
ID AAU02694 standard; Peptide; 9 AA.
XX
AC AAU02694;
XX
DT 29-AUG-2001 (first entry)
XX
DE CDR region of anti-adipocyte antibody heavy chain, FAT 58.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.

XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
DR N-PSDB; AAS03470.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
Example 7; Page 78; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 9 AA;

Query Match 63.6%; Score 35; DB 22; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDSSGIHV 10
|||||:
Db 2 rdssgyhi 9

RESULT 11
AAY95197
ID AAY95197 standard; Peptide; 9 AA.
XX
AC AAY95197;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-1 VL CDR3.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-1;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR3;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Claim 21; Fig 5; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 3 (CDR3) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-1 (see AAY95198), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 9 AA;

Query Match 61.8%; Score 34; DB 21; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIH 9
|||||| |
Db 2 srdssgnh 9

RESULT 12
AAY95218
ID AAY95218 standard; Peptide; 9 AA.
XX
AC AAY95218;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human HIb-3 VL CDR3.
XX
KW Variable light chain; single chain antibody; scFv; human; HIb-3;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR3;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX

PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Claim 21; Fig 7; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 3 (CDR3) of the light chain variable region (VL) of human
CC single chain antibody (scFv) HIb-3 (see AAY95219), which is directed
CC against platelet glycoprotein Ib (GPIb). The HIb series of scFv
CC was isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the HIb scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 9 AA;

Query Match 61.8%; Score 34; DB 21; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SRDSSGIH 9
||||||:|
Db 2 srdssgnh 9

RESULT 13
AAR88543
ID AAR88543 standard; peptide; 10 AA.
XX
AC AAR88543;
XX
DT 09-SEP-1996 (first entry)
XX
DE Varicella zoster gE glycoprotein residues 126-135.
XX
KW Glycoprotein; gE; VZV; antibody; gB; immunoreactive; immune response;
KW infection; diagnosis; therapy.
XX
OS Varicella-zoster virus.
XX
PN WO9601900-A1.
XX
PD 25-JAN-1996.
XX
PF 03-JUL-1995; 95WO-GB01566.
XX
PR 07-JUL-1994; 94GB-0013751.
XX
PA (BRBI-) BRITISH BIOTECH PHARM LTD.
XX
PI Fowler WJ, Garcia-valcarcel Munoz-repiso M, Harper DR;
PI Layton GT;
XX
DR WPI; 1996-097630/10.
XX
PT New isolated Varicella Zoster gE polypeptide(s) - used to develop
PT products for use in vaccines, passive immunisation and diagnosis
PT involving VZV infection
XX
PS Claim 3; Page 37; 47pp; English.
XX
CC AAR88522-R88549 represent fragments of the Varicella-Zoster virus (VZV)
CC gE glycoprotein. This sequence represents residues 126-135 of gE.
CC These sequences are used to create antibodies against the VZV gE
CC glycoprotein. gE is one of six glycoproteins encoded by the VZV genome.
CC From these six proteins, gE and gB are the major immunoreactive
CC glycoproteins. These sequences can be used for stimulating an immune
CC response against VZV infection. These peptides can also be used for
CC determining the presence of anti-VZV gE antibodies in a sample, and in
CC the diagnosis of VZV infection. The antibodies against these sequences
CC can be used for passive immunisation treatment, and in diagnostic
CC applications. This sequence contains the major VZV gE immunodominant
CC epitope and allows the development of products which can produce an
CC enhanced and broader immune response.
XX
SQ Sequence 10 AA;

Query Match 58.2%; Score 32; DB 17; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.7;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DSSGIHVV 11
| :||||:
Db 3 ddtgihvi 10

RESULT 14
AAU08356
ID AAU08356 standard; peptide; 11 AA.
XX
AC AAU08356;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antibody light chain variable region CDR3 #4.
XX
KW Antibody; light chain; CDR2; complementarity determining region; OPGbp;
KW osteopathic; osteoprotegrin binding protein; osteoclast formation;
KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
KW steroid-induced osteoporosis.
XX
OS Synthetic.
XX
PN WO200162932-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US05973.
XX
PR 23-FEB-2000; 2000US-0511139.
PR 22-FEB-2001; 2001US-0791153.
XX
PA (AMGE-) AMGEN INC.
XX
PI Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
XX
DR WPI; 2001-557706/62.
XX
PT Antibodies that bind antagonistically to osteoprotegrin binding
PT protein, useful for treating osteoporosis, metastasis of cancer to
PT bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT steroid-induced osteoporosis -
XX
PS Claim 14; Page 129; 239pp; English.
XX

CC The invention relates to an antibody or antigen binding domain (or
CC fragment, variant or derivative), which binds to an osteoprotegrin
CC binding protein (OPGbp) and which is an antagonistic antibody.
CC The antibody or antigen binding domain may be administered to inhibit
CC osteoclast formation or activation, inhibit bone resorption in a mammal,
CC prevent or treat loss of bone mass in a mammal and to prevent or treat
CC tumour cell growth in bone. The loss of bone mass results from
CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC present sequence is an antibody light chain variable region
CC complementarity determining region, CDR3, which can be incorporated into
CC an antibody/antigen binding domain of the invention.
XX
SQ Sequence 11 AA;

Query Match 58.2%; Score 32; DB 22; Length 11;
Best Local Similarity 70.0%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
| |||| :||
Db 2 stdssgtyvv 11

RESULT 15
AAW62282
ID AAW62282 standard; peptide; 11 AA.
XX
AC AAW62282;
XX
DT 24-SEP-1998 (first entry)
XX
DE Synthetic immunoglobulin TVG 405 light chain CDR3 peptide.
XX
KW HPV16; human papilloma virus; epithelial tumour; cervical cancer;
KW precancerous cervical lesion; screening; detection; infection; cervix;
KW HPV E4; immunoglobulin; antibody.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO9825145-A1.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-GB03321.
XX
PR 05-SEP-1997; 97GB-0018745.
PR 03-DEC-1996; 96GB-0025142.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Doorbar J;
XX
DR WPI; 1998-333497/29.
XX
PT Detecting papilloma virus infection using molecule binding to E4
PT protein - useful, e.g. in screening for pre-cancerous cervical
PT lesions and to determine type(s) of human papilloma virus infecting
PT human patients
XX
PS Example 2; Page 17; 52pp; English.
XX
CC A new method has been developed for detecting a papilloma virus infection
CC in an organism. The method comprises: (i) obtaining a sample of cells
CC from the potential infection site; (ii) contacting the cells with a
CC molecule binding specifically to papilloma virus E4 protein, and (iii)
CC monitoring the binding. The method is useful to detect papilloma virus
CC infections in organisms (especially mammals) and especially HPV
CC infections (e.g. with HPV16, 18, 33, 35, 45, 51, 56, 58 or 61) in humans.
CC Papilloma viruses cause epithelial tumours in humans varying in severity
CC depending on the infection site and HPV type involved. The method is
CC particularly useful to determine papilloma infection in the mammalian
CC cervix and especially to screen for pre-cancerous cervical lesions in
CC humans, since over 90% of cervical carcinoma patients show cervical HPV
CC infection. It is also useful to determine the type(s) of HPV infection in
CC a patient, by using a molecule binding specifically to a subset of HPV E4
CC proteins. This is important, since progression to malignant disease (and
CC hence clinical prognosis) is dependent on HPV type. Molecules capable of
CC binding E4 are also useful to target anticancer/antiviral agents capable
CC of destroying papilloma viruses and/or papilloma virus-infected cells.
CC The present sequence represents a synthetic immunoglobulin TVG 405 light
CC chain CDR3 peptide, from an example of the present invention.
XX
SQ Sequence 11 AA;

Query Match 54.5%; Score 30; DB 19; Length 11;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SRDSSGIHVV 11
|||||| : |
Db 2 srdssggnav 11

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